GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 12, 2005, 10:20:03 ; Search time 166 Seconds
(without alignments)
35.086 Million cell updates/sec

Title: US-09-155-076-1
Perfect score: 87
Sequence: 1 AEFHRWSSYMVHWK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1854112 seqs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	87	100.0	40	10	US-09-998-042-2	Sequence 2, Appli
3	87	100.0	44	9	US-09-155-076-6	Sequence 6, Appli
4	87	100.0	44	9	US-09-155-076-8	Sequence 8, Appli
5	87	100.0	44	9	US-09-155-076-9	Sequence 9, Appli
6	87	100.0	53	9	US-09-155-076-10	Sequence 10, Appl
7	87	100.0	54	9	US-09-155-076-7	Sequence 7, Appli
8	87	100.0	67	10	US-09-998-042-8	Sequence 8, Appli
9	87	100.0	614	15	US-10-116-275-258	Sequence 258, App
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11	80	92.0	576	18	US-10-503-691-4	Sequence 4, Appli
12	78	89.7	27	10	US-09-998-042-3	Sequence 3, Appli
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ALIGNMENTS

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RESULT 1
US-09-155-076-1
; Sequence 1, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
;  APPLICANT: Greenfield et al., Susan A.
;  TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
;  TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
;  FILE REFERENCE: 98-0967*/WMC/00263
;  CURRENT APPLICATION NUMBER: US/09/155,076A
;  CURRENT FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;    LENGTH: 14
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: PEPTIDE
US-09-155-076-1

  Query Match             100.0%;  Score 87;  DB 9;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
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RESULT 2
US-09-998-042-2
; Sequence 2, Application US/09998042
; Publication No. US20030036632A1
; GENERAL INFORMATION:
;  APPLICANT: YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW
;  TITLE OF INVENTION: ACETYLCHOLINESTERASE-DERIVED PEPTIDE AND USES THEREOF
;  FILE REFERENCE: 7811/WO/99
;  CURRENT APPLICATION NUMBER: US/09/998,042
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENCE
US-09-998-042-2

  Query Match             100.0%;  Score 87;  DB 10;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 7e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         12 AEFHRWSSYMVHWK 25


RESULT 3
US-09-155-076-6
; Sequence 6, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
;  APPLICANT: Greenfield et al., Susan A.
;  TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
;  TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
;  FILE REFERENCE: 98-0967*/WMC/00263
;  CURRENT APPLICATION NUMBER: US/09/155,076A
;  CURRENT FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 44
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
US-09-155-076-6

  Query Match             100.0%;  Score 87;  DB 9;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         16 AEFHRWSSYMVHWK 29


RESULT 4
US-09-155-076-8
; Sequence 8, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
;  APPLICANT: Greenfield et al., Susan A.
;  TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
;  TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
;  FILE REFERENCE: 98-0967*/WMC/00263
;  CURRENT APPLICATION NUMBER: US/09/155,076A
;  CURRENT FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 44
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
US-09-155-076-8

  Query Match             100.0%;  Score 87;  DB 9;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         16 AEFHRWSSYMVHWK 29


RESULT 5
US-09-155-076-9
; Sequence 9, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
;  APPLICANT: Greenfield et al., Susan A.
;  TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
;  TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
;  FILE REFERENCE: 98-0967*/WMC/00263
;  CURRENT APPLICATION NUMBER: US/09/155,076A
;  CURRENT FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 44
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
US-09-155-076-9

  Query Match             100.0%;  Score 87;  DB 9;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         16 AEFHRWSSYMVHWK 29


RESULT 6
US-09-155-076-10
; Sequence 10, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
;  APPLICANT: Greenfield et al., Susan A.
;  TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
;  TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
;  FILE REFERENCE: 98-0967*/WMC/00263
;  CURRENT APPLICATION NUMBER: US/09/155,076A
;  CURRENT FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 53
;   TYPE: PRT
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;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
US-09-155-076-10

  Query Match             100.0%;  Score 87;  DB 9;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         25 AEFHRWSSYMVHWK 38


RESULT 7
US-09-155-076-7
; Sequence 7, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
;  APPLICANT: Greenfield et al., Susan A.
;  TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
;  TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
;  FILE REFERENCE: 98-0967*/WMC/00263
;  CURRENT APPLICATION NUMBER: US/09/155,076A
;  CURRENT FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 54
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
US-09-155-076-7

  Query Match             100.0%;  Score 87;  DB 9;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 9e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         26 AEFHRWSSYMVHWK 39


RESULT 8
US-09-998-042-8
; Sequence 8, Application US/09998042
; Publication No. US20030036632A1
; GENERAL INFORMATION:
;  APPLICANT: YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW
;  TITLE OF INVENTION: ACETYLCHOLINESTERASE-DERIVED PEPTIDE AND USES THEREOF
;  FILE REFERENCE: 7811/WO/99
;  CURRENT APPLICATION NUMBER: US/09/998,042
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:ASP - peptide
;   OTHER INFORMATION: for two-hybrid screen
US-09-998-042-8

  Query Match             100.0%;  Score 87;  DB 10;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         39 AEFHRWSSYMVHWK 52


RESULT 9
US-10-116-275-258
; Sequence 258, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
;  APPLICANT: Elan Pharmaceutical Technology
;  APPLICANT:  O'Mahony, Daniel J.
;  APPLICANT:  Brayden, David
;  APPLICANT:  Byrne, Daragh
;  APPLICANT:  Lambkin, Imelda
;  APPLICANT:  Higgins, Lisa
;  TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
;  TITLE OF INVENTION:  Compositions Targeting Peyer's Patches and M Cell Receptors
;  FILE REFERENCE: E1067/20087
;  CURRENT APPLICATION NUMBER: US/10/116,275
;  CURRENT FILING DATE:  2002-10-04
;  NUMBER OF SEQ ID NOS: 349
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 258
;   LENGTH: 614
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-116-275-258

  Query Match             100.0%;  Score 87;  DB 15;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00075;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 10
US-10-503-643-3
; Sequence 3, Application US/10503643
; Publication No. US20050176117A1
; GENERAL INFORMATION:
;  APPLICANT: Robyn Joyce Russell
;  APPLICANT:  Rama Heidari
;  APPLICANT:  Alan Devonshire
;  APPLICANT:  Susan Jane Dorrian
;  APPLICANT:  John Graham Oakeshott
;  TITLE OF INVENTION: Degradation of hydrophobic ester pesticides and toxins
;  FILE REFERENCE: 69-04
;  CURRENT APPLICATION NUMBER: US/10/503,643
;  CURRENT FILING DATE:  2004-08-04
;  PRIOR APPLICATION NUMBER: PCT/AU02/00114
;  PRIOR FILING DATE: 2002-02-06
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Torpedo californica
US-10-503-643-3

  Query Match             92.0%;  Score 80;  DB 18;  Length 576;
  Best Local Similarity   92.3%;  Pred. No. 0.0064;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              |||||||||:|||
Db        549 EFHRWSSYMMHWK 561


RESULT 11
US-10-503-691-4
; Sequence 4, Application US/10503691
; Publication No. US20050176118A1
; GENERAL INFORMATION:
;  APPLICANT: John Graham Oakeshott
```

```
;  APPLICANT:  Alan Devonshire
;  APPLICANT:  Christopher Wayne Coppin
;  APPLICANT:  Rama Heidari
;  APPLICANT:  Susan Jane Dorrian
;  APPLICANT:  Robyn Joyce Russell
;  TITLE OF INVENTION: Esterases with lipase activity
;  FILE REFERENCE: 70-04
;  CURRENT APPLICATION NUMBER: US/10/503,691
;  CURRENT FILING DATE:  2004-08-04
;  PRIOR APPLICATION NUMBER: PCT/AU02/00113
;  PRIOR FILING DATE: 2002-02-06
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Torpedo californica
US-10-503-691-4

  Query Match             92.0%;  Score 80;  DB 18;  Length 576;
  Best Local Similarity   92.3%;  Pred. No. 0.0064;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              |||||||||:|||
Db        549 EFHRWSSYMMHWK 561


RESULT 12
US-09-998-042-3
; Sequence 3, Application US/09998042
; Publication No. US20030036632A1
; GENERAL INFORMATION:
;  APPLICANT: YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW
;  TITLE OF INVENTION: ACETYLCHOLINESTERASE-DERIVED PEPTIDE AND USES THEREOF
;  FILE REFERENCE: 7811/WO/99
;  CURRENT APPLICATION NUMBER: US/09/998,042
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 27
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-998-042-3

  Query Match             89.7%;  Score 78;  DB 10;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0.00084;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FHRWSSYMVHWK 14
              ||||||||||||
Db          1 FHRWSSYMVHWK 12


RESULT 13
US-09-748-739A-23
; Sequence 23, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-09-748-739A-23

  Query Match             74.7%;  Score 65;  DB 9;  Length 574;
  Best Local Similarity   71.4%;  Pred. No. 0.73;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | |||||:||: ||
Db        545 AGFHRWSNYMMDWK 558


RESULT 14
US-10-032-233-50
; Sequence 50, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-10-032-233-50

  Query Match             74.7%;  Score 65;  DB 14;  Length 574;
  Best Local Similarity   71.4%;  Pred. No. 0.73;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | |||||:||: ||
Db        545 AGFHRWSNYMMDWK 558


RESULT 15
US-10-413-432-50
; Sequence 50, Application US/10413432
; Publication No. US20040120939A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variant
;  TITLE OF INVENTION:  Polypeptides with Increased Catalytic Efficiency and Methods
;  TITLE OF INVENTION:  of Use
;  FILE REFERENCE: P-IX 5510
;  CURRENT APPLICATION NUMBER: US/10/413,432
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: US 10/324,466
;  PRIOR FILING DATE: 2002-12-20
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-10-413-432-50

  Query Match             74.7%;  Score 65;  DB 16;  Length 574;
  Best Local Similarity   71.4%;  Pred. No. 0.73;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | |||||:||: ||
Db        545 AGFHRWSNYMMDWK 558


RESULT 16
```

```
US-10-324-466-50
; Sequence 50, Application US/10324466
; Publication No. US20040121970A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variant
;  TITLE OF INVENTION:  Polypeptides with Increased Catalytic Efficiency and Methods
;  TITLE OF INVENTION:  of Use
;  FILE REFERENCE: P-IX 5555
;  CURRENT APPLICATION NUMBER: US/10/324,466
;  CURRENT FILING DATE:  2002-12-20
;  PRIOR APPLICATION NUMBER: US 10/032,233
;  PRIOR FILING DATE: 2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 50
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-10-324-466-50

  Query Match             74.7%;  Score 65;  DB 16;  Length 574;
  Best Local Similarity   71.4%;  Pred. No. 0.73;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | |||||:||: ||
Db        545 AGFHRWSNYMMDWK 558


RESULT 17
US-09-155-076-15
; Sequence 15, Application US/09155076A
; Patent No. US20020054870A1
; GENERAL INFORMATION:
;  APPLICANT: Greenfield et al., Susan A.
;  TITLE OF INVENTION: PEPTIDE FROM SOLUBLE FORM OF ACETYLCHOLINESTERASE,
;  TITLE OF INVENTION: ACTIVE AS A CALCIUM CHANNEL MODULATOR
;  FILE REFERENCE: 98-0967*/WMC/00263
;  CURRENT APPLICATION NUMBER: US/09/155,076A
;  CURRENT FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
US-09-155-076-15

  Query Match             71.3%;  Score 62;  DB 9;  Length 14;
  Best Local Similarity   64.3%;  Pred. No. 0.074;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db          1 AGFHRWNNYMMDWK 14


RESULT 18
US-10-728-723-52
; Sequence 52, Application US/10728723
; Publication No. US20050136044A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants That
;  TITLE OF INVENTION:  Alter the Activity of Chemotherapeutic Agents
;  FILE REFERENCE: 66797-395
;  CURRENT APPLICATION NUMBER: US/10/728,723
;  CURRENT FILING DATE:  2003-12-04
;  PRIOR APPLICATION NUMBER: US 10/310,666
;  PRIOR FILING DATE: 2002-12-04
;  NUMBER OF SEQ ID NOS: 204
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
;   LENGTH: 573
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic butyrylcholinesterase variant
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(573)
;   OTHER INFORMATION: Xaa = Ala
US-10-728-723-52

  Query Match             71.3%;  Score 62;  DB 18;  Length 573;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        544 AGFHRWNNYMMDWK 557


RESULT 19
US-10-728-723-92
; Sequence 92, Application US/10728723
; Publication No. US20050136044A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants That
;  TITLE OF INVENTION:  Alter the Activity of Chemotherapeutic Agents
;  FILE REFERENCE: 66797-395
;  CURRENT APPLICATION NUMBER: US/10/728,723
;  CURRENT FILING DATE:  2003-12-04
;  PRIOR APPLICATION NUMBER: US 10/310,666
;  PRIOR FILING DATE: 2002-12-04
;  NUMBER OF SEQ ID NOS: 204
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
;   LENGTH: 573
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic butyrylcholinesterase variant
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(573)
;   OTHER INFORMATION: Xaa = Ala
US-10-728-723-92

  Query Match             71.3%;  Score 62;  DB 18;  Length 573;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        544 AGFHRWNNYMMDWK 557


RESULT 20
US-10-728-723-110
; Sequence 110, Application US/10728723
; Publication No. US20050136044A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants That
;  TITLE OF INVENTION:  Alter the Activity of Chemotherapeutic Agents
;  FILE REFERENCE: 66797-395
;  CURRENT APPLICATION NUMBER: US/10/728,723
```

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;  CURRENT FILING DATE:  2003-12-04
;  PRIOR APPLICATION NUMBER: US 10/310,666
;  PRIOR FILING DATE: 2002-12-04
;  NUMBER OF SEQ ID NOS: 204
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110
;   LENGTH: 573
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic butyrylcholinesterase variant
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(573)
;   OTHER INFORMATION: Xaa = Ala
US-10-728-723-110

  Query Match             71.3%;  Score 62;  DB 18;  Length 573;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        544 AGFHRWNNYMMDWK 557


RESULT 21
US-09-748-739A-4
; Sequence 4, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-4

  Query Match             71.3%;  Score 62;  DB 9;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 22
US-09-748-739A-6
; Sequence 6, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-6

  Query Match             71.3%;  Score 62;  DB 9;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 23
US-09-748-739A-8
; Sequence 8, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-8

  Query Match             71.3%;  Score 62;  DB 9;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 24
US-09-748-739A-17
; Sequence 17, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-748-739A-17

  Query Match             71.3%;  Score 62;  DB 9;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558
```

```
RESULT 25
US-09-748-739A-18
; Sequence 18, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-748-739A-18

  Query Match             71.3%;  Score 62;  DB 9;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 26
US-09-748-739A-19
; Sequence 19, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-748-739A-19

  Query Match             71.3%;  Score 62;  DB 9;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 27
US-09-748-739A-20
; Sequence 20, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-748-739A-20

  Query Match             71.3%;  Score 62;  DB 9;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 28
US-09-748-739A-21
; Sequence 21, Application US/09748739A
; Patent No. US20020119489A1
; GENERAL INFORMATION:
;  APPLICANT: Lockridge, Oksana
;  APPLICANT:  Watkins, Jeffry D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 4143
;  CURRENT APPLICATION NUMBER: US/09/748,739A
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Equus caballus
US-09-748-739A-21

  Query Match             71.3%;  Score 62;  DB 9;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 29
US-09-997-209-89
; Sequence 89, Application US/09997209
; Publication No. US20030096401A1
; GENERAL INFORMATION:
;  APPLICANT: Huse, William D.
;  TITLE OF INVENTION: Eukaryotic Expression Libraries and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: P-IX 5066
;  CURRENT APPLICATION NUMBER: US/09/997,209
;  CURRENT FILING DATE:  2001-11-28
;  PRIOR APPLICATION NUMBER: US 09/724,762
;  PRIOR FILING DATE: 2000-11-28
;  NUMBER OF SEQ ID NOS: 90
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-997-209-89

  Query Match             71.3%;  Score 62;  DB 10;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558
```

```
RESULT 30
US-10-032-233-2
; Sequence 2, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-2

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 31
US-10-032-233-4
; Sequence 4, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-4

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 32
US-10-032-233-6
; Sequence 6, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-6

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 33
US-10-032-233-8
; Sequence 8, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-8

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 34
US-10-032-233-10
; Sequence 10, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Butyrylcholinesterase variant
```

```
US-10-032-233-10

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 35
US-10-032-233-12
; Sequence 12, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-12

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 36
US-10-032-233-14
; Sequence 14, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-14

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 37
US-10-032-233-16
; Sequence 16, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-16

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 38
US-10-032-233-18
; Sequence 18, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-18

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 39
US-10-032-233-20
; Sequence 20, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
```

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;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;    LENGTH: 574
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-20

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 40
US-10-032-233-22
; Sequence 22, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
;    LENGTH: 574
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-22

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 41
US-10-032-233-24
; Sequence 24, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;    LENGTH: 574
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-24

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 42
US-10-032-233-26
; Sequence 26, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;    LENGTH: 574
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-26

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 43
US-10-032-233-28
; Sequence 28, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
;    LENGTH: 574
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-28

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 44
US-10-032-233-30
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```
; Sequence 30, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-30

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
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RESULT 45
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; Sequence 32, Application US/10032233
; Publication No. US20030153062A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffry D.
;  APPLICANT:  Pancook, James D.
;  TITLE OF INVENTION: Butyrylcholinesterase Variants with
;  TITLE OF INVENTION:  Increased Catalytic Efficiency and Methods of Use
;  FILE REFERENCE: P-IX 4642
;  CURRENT APPLICATION NUMBER: US/10/032,233
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 574
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Butyrylcholinesterase variant
US-10-032-233-32

  Query Match             71.3%;  Score 62;  DB 14;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 1.9;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

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Search completed: October 12, 2005, 10:34:48
Job time : 169 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 12, 2005, 10:15:43 ; Search time 41 Seconds
(without alignments)
25.490 Million cell updates/sec

Title: US-09-155-076-1
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	87	100.0	45	2	US-08-370-156-8	Sequence 8, Appli
4	87	100.0	45	3	US-08-990-065-21	Sequence 21, Appl
5	87	100.0	45	3	US-08-975-084-5	Sequence 5, Appli
6	87	100.0	45	4	US-09-380-532-11	Sequence 11, Appl
7	87	100.0	614	1	US-07-732-962A-2	Sequence 2, Appli
8	87	100.0	614	2	US-08-370-156-2	Sequence 2, Appli
9	87	100.0	614	3	US-08-446-100-19	Sequence 19, Appl
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11	87	100.0	614	3	US-08-446-100-21	Sequence 21, Appl
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13	87	100.0	614	3	US-08-446-100-23	Sequence 23, Appl
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18	87	100.0	645	4	US-09-949-016-7064	Sequence 7064, Ap
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83	40	46.0	146	1	US-08-899-575-155	Sequence 155, App
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134	38	43.7	124	1	US-08-899-575-132	Sequence 132, App
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146	38	43.7	125	5	PCT-US95-08743-128	Sequence 128, App
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182	37	42.5	110	3	US-08-545-809A-129	Sequence 129, App
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ALIGNMENTS

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RESULT 1
US-08-370-156-25
; Sequence 25, Application US/08370156
; Patent No. 5932780
;  GENERAL INFORMATION:
;    APPLICANT:  Soreq, Hermona
;    APPLICANT:  Zakut, Haim
;    APPLICANT:  Shani, Moshe
;    TITLE OF INVENTION:  TRANSGENIC ANIMAL ASSAY SYSTEM FOR
;    TITLE OF INVENTION:  ANTICHOLINESTERASE SUBSTANCES
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reising, Ethington, Barnard & Perry
;      STREET:  P.O. Box 4390
;      CITY:  Troy
;      STATE:  Michigan
;      COUNTRY:  US
;      ZIP:  48099
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/370,156
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kohn, Kenneth I.
;      REGISTRATION NUMBER:  30,955
;      REFERENCE/DOCKET NUMBER:  P-307 (Mulford)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (810) 689-3500
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;      TELEFAX:  (810) 689-4071
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-370-156-25

  Query Match             100.0%;  Score 87;  DB 2;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         12 AEFHRWSSYMVHWK 25


RESULT 2
US-08-370-156-7
; Sequence 7, Application US/08370156
; Patent No. 5932780
;  GENERAL INFORMATION:
;    APPLICANT:  Soreq, Hermona
;    APPLICANT:  Zakut, Haim
;    APPLICANT:  Shani, Moshe
;    TITLE OF INVENTION:  TRANSGENIC ANIMAL ASSAY SYSTEM FOR
;    TITLE OF INVENTION:  ANTICHOLINESTERASE SUBSTANCES
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reising, Ethington, Barnard & Perry
;      STREET:  P.O. Box 4390
;      CITY:  Troy
;      STATE:  Michigan
;      COUNTRY:  US
;      ZIP:  48099
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/370,156
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kohn, Kenneth I.
;      REGISTRATION NUMBER:  30,955
;      REFERENCE/DOCKET NUMBER:  P-307 (Mulford)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (810) 689-3500
;      TELEFAX:  (810) 689-4071
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-370-156-7

  Query Match             100.0%;  Score 87;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         17 AEFHRWSSYMVHWK 30


RESULT 3
US-08-370-156-8
; Sequence 8, Application US/08370156
; Patent No. 5932780
;  GENERAL INFORMATION:
;    APPLICANT:  Soreq, Hermona
;    APPLICANT:  Zakut, Haim
;    APPLICANT:  Shani, Moshe
;    TITLE OF INVENTION:  TRANSGENIC ANIMAL ASSAY SYSTEM FOR
;    TITLE OF INVENTION:  ANTICHOLINESTERASE SUBSTANCES
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reising, Ethington, Barnard & Perry
;      STREET:  P.O. Box 4390
;      CITY:  Troy
;      STATE:  Michigan
;      COUNTRY:  US
;      ZIP:  48099
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/370,156
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kohn, Kenneth I.
;      REGISTRATION NUMBER:  30,955
;      REFERENCE/DOCKET NUMBER:  P-307 (Mulford)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (810) 689-3500
;      TELEFAX:  (810) 689-4071
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-370-156-8

  Query Match             100.0%;  Score 87;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         17 AEFHRWSSYMVHWK 30


RESULT 4
US-08-990-065-21
; Sequence 21, Application US/08990065
; Patent No. 6121046
;  GENERAL INFORMATION:
;    APPLICANT:  Soreq, Hermona
;    APPLICANT:  Seidman, Shlomo
;    APPLICANT:  Eckstein, Fritz
;    APPLICANT:  Friedman, Alon
;    APPLICANT:  Kaufer, Daniela
;    TITLE OF INVENTION:  SYNTHETIC ANTISENSE
;    TITLE OF INVENTION:  OLIGODEOXYNUCLEOTIDES AND PHARMACEUTICAL COMPOSITIONS
;    TITLE OF INVENTION:  CONTAINING THEM
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kohn & Associates
;      STREET:  30500 No. 6121046thwestern Hwy.  Suite 410
;      CITY:  Farmington Hills
;      STATE:  Michigan
;      COUNTRY:  U.S.
;      ZIP:  48334
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/990,065
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/850,347
;      FILING DATE:  02-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/318,826
;      FILING DATE:  01-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Montgomery, Ilene N.
;      REGISTRATION NUMBER:  38,972
;      REFERENCE/DOCKET NUMBER:  2391.00086
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (248) 539-5050
;      TELEFAX:  (248) 539-5055
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-990-065-21

  Query Match             100.0%;  Score 87;  DB 3;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         17 AEFHRWSSYMVHWK 30


RESULT 5
US-08-975-084-5
; Sequence 5, Application US/08975084
; Patent No. 6258780
;  GENERAL INFORMATION:
;    APPLICANT:  SOREQ, Hermona
;    APPLICANT:  FRIEDMAN, Alon
;    APPLICANT:  SEIDMAN, Shlomo
;    APPLICANT:  KAUFER, Daniela
;    TITLE OF INVENTION:  A METHOD AND COMPOSITION FOR ENABLING
;    TITLE OF INVENTION:  PASSAGE THROUGH THE BLOOD-BRAIN-BARRIER
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kohn & Associates
;      STREET:  30500 No. 6258780thwestern Hwy., Suite 410
;      CITY:  Farminton Hills
;      STATE:  Michigan
;      COUNTRY:  US
;      ZIP:  48334
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/975,084
;      FILING DATE:  11-NOV-1997
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Montgomery, Ilene N.
;      REGISTRATION NUMBER:  38,972
;      REFERENCE/DOCKET NUMBER:  2391.00082
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (248) 539-5050
;      TELEFAX:  (248) 539-5055
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  45 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-975-084-5

  Query Match             100.0%;  Score 87;  DB 3;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         17 AEFHRWSSYMVHWK 30


RESULT 6
US-09-380-532-11
; Sequence 11, Application US/09380532
; Patent No. 6475998
;  GENERAL INFORMATION:
;       APPLICANT: Soreq, Hermona
;                  Seidman, Shlomo
;                  Shohami, Esther
;       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
;                           TREATMENT OF INJURY TO THE CENTRAL NERVOUS SYSTEM
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Kohn & Associates
;            STREET: 30500 No. 6475998thwestern Hwy.
;            CITY: Farmington Hills
;            STATE: Michigan
;            COUNTRY: US
;            ZIP: 48334
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/380,532
;            FILING DATE: 12-No. 6475998-1999
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Montgomery, Ilene N.
;            REGISTRATION NUMBER: 38,972
;            REFERENCE/DOCKET NUMBER: 2391.00089
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (248) 539-5050
;            TELEFAX: (248) 539-5055
;  INFORMATION FOR SEQ ID NO: 11:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 45 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: not relevant
;            TOPOLOGY: not relevant
;       MOLECULE TYPE: peptide
;       HYPOTHETICAL: NO
;       ORIGINAL SOURCE:
;            ORGANISM: Homo sapiens
;       SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-380-532-11

  Query Match             100.0%;  Score 87;  DB 4;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         17 AEFHRWSSYMVHWK 30
```

```
RESULT 7
US-07-732-962A-2
; Sequence 2, Application US/07732962A
; Patent No. 5248604
;  GENERAL INFORMATION:
;    APPLICANT:  Fischer, Meir
;    TITLE OF INVENTION:  EXPRESSION OF ENZYMATICALLY ACTIVE
;    TITLE OF INVENTION:  RECOMBINANT HUMAN ACETYLCHOLINESTERASE
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John P. White, Esq.
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/732,962A
;      FILING DATE:  19910722
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  39304/JPW/LSW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 977-9550
;      TELEFAX:  (212) 664-0525
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  614 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-732-962A-2

  Query Match             100.0%;  Score 87;  DB 1;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00024;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 8
US-08-370-156-2
; Sequence 2, Application US/08370156
; Patent No. 5932780
;  GENERAL INFORMATION:
;    APPLICANT:  Soreq, Hermona
;    APPLICANT:  Zakut, Haim
;    APPLICANT:  Shani, Moshe
;    TITLE OF INVENTION:  TRANSGENIC ANIMAL ASSAY SYSTEM FOR
;    TITLE OF INVENTION:  ANTICHOLINESTERASE SUBSTANCES
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Reising, Ethington, Barnard & Perry
;      STREET:  P.O. Box 4390
;      CITY:  Troy
;      STATE:  Michigan
;      COUNTRY:  US
;      ZIP:  48099
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/370,156
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kohn, Kenneth I.
;      REGISTRATION NUMBER:  30,955
;      REFERENCE/DOCKET NUMBER:  P-307 (Mulford)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (810) 689-3500
;      TELEFAX:  (810) 689-4071
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  614 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-370-156-2

  Query Match             100.0%;  Score 87;  DB 2;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00024;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 9
US-08-446-100-19
; Sequence 19, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  614 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
```

```
US-08-446-100-19

  Query Match             100.0%;  Score 87;  DB 3;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00024;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 10
US-08-446-100-20
; Sequence 20, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  614 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-20

  Query Match             100.0%;  Score 87;  DB 3;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00024;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 11
US-08-446-100-21
; Sequence 21, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  614 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-21

  Query Match             100.0%;  Score 87;  DB 3;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00024;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 12
US-08-446-100-22
; Sequence 22, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
```

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;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  614 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-22

  Query Match             100.0%;  Score 87;  DB 3;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00024;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 13
US-08-446-100-23
; Sequence 23, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  614 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-23

  Query Match             100.0%;  Score 87;  DB 3;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00024;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 14
US-08-446-100-25
; Sequence 25, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  614 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-25

  Query Match             100.0%;  Score 87;  DB 3;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00024;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 15
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US-08-814-095-2
; Sequence 2, Application US/08814095
; Patent No. 6025183
;  GENERAL INFORMATION:
;    APPLICANT:  Soreq, Hermona
;    APPLICANT:  Zakut, Haim
;    APPLICANT:  Shani, Moshe
;    TITLE OF INVENTION:  TRANSGENIC ANIMAL ASSAY SYSTEM FOR
;    TITLE OF INVENTION:  ANTI-CHOLINESTERASE SUBSTNACES
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  KOHN & ASSOCIATES
;      STREET:  30500 No. 6025183thwestern Highway, Suite 410
;      CITY:  Farmington Hills
;      STATE:  Michigan
;      COUNTRY:  U.S.
;      ZIP:  48334
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/814,095
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Montgomery, Ilene N.
;      REGISTRATION NUMBER:  38,972
;      REFERENCE/DOCKET NUMBER:  2391.00066
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (248) 539-5050
;      TELEFAX:  (248) 539-5055
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  614 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-08-814-095-2

  Query Match             100.0%;  Score 87;  DB 3;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00024;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 16
PCT-US92-06106-2
; Sequence 2, Application PC/TUS9206106
;  GENERAL INFORMATION:
;    APPLICANT:  Fischer, Meir
;    TITLE OF INVENTION:  ENZYMATICALLY ACTIVE RECOMBINANT HUMAN
;    TITLE OF INVENTION:  ACETYLCHOLINESTERASE AND USES THEREOF
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John P. White, Esq.
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/06106
;      FILING DATE:  19920722
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  39304-B-PCT/JPW/EAB
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 977-9550
;      TELEFAX:  (212) 664-0525
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  614 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US92-06106-2

  Query Match             100.0%;  Score 87;  DB 5;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00024;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 17
US-09-949-016-7063
; Sequence 7063, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7063
;   LENGTH: 645
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7063

  Query Match             100.0%;  Score 87;  DB 4;  Length 645;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        617 AEFHRWSSYMVHWK 630


RESULT 18
US-09-949-016-7064
; Sequence 7064, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
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;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7064
;   LENGTH: 645
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7064

  Query Match             100.0%;  Score 87;  DB 4;  Length 645;
  Best Local Similarity   100.0%;  Pred. No. 0.00025;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        617 AEFHRWSSYMVHWK 630


RESULT 19
US-08-348-920-1
; Sequence 1, Application US/08348920
; Patent No. 5695750
;  GENERAL INFORMATION:
;    APPLICANT:  Doctor, Bhupandra P.
;    APPLICANT:  Maxwell, Donald
;    APPLICANT:  Saxena, Ashima
;    APPLICANT:  Radic, Zoran
;    APPLICANT:  Taylor, Palmer
;    TITLE OF INVENTION:  Compositions for Use to Deactivate
;    TITLE OF INVENTION:  Organophosphates
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John F. Moran
;      STREET:  Off. of Command Judge Adv., HQ USAMRDC, Fort
;      STREET:  Detrick
;      CITY:  Frederick
;      STATE:  MD
;      COUNTRY:  US
;      ZIP:  21702-5012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/348,920
;      FILING DATE:  25-NOV-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  doc348,920
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 619-7807
;      TELEFAX:  301-619-7714
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  575 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-348-920-1

  Query Match             92.0%;  Score 80;  DB 1;  Length 575;
  Best Local Similarity   92.3%;  Pred. No. 0.002;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              |||||||||:|||
Db        548 EFHRWSSYMMHWK 560


RESULT 20
US-08-348-920-2
; Sequence 2, Application US/08348920
; Patent No. 5695750
;  GENERAL INFORMATION:
;    APPLICANT:  Doctor, Bhupandra P.
;    APPLICANT:  Maxwell, Donald
;    APPLICANT:  Saxena, Ashima
;    APPLICANT:  Radic, Zoran
;    APPLICANT:  Taylor, Palmer
;    TITLE OF INVENTION:  Compositions for Use to Deactivate
;    TITLE OF INVENTION:  Organophosphates
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John F. Moran
;      STREET:  Off. of Command Judge Adv., HQ USAMRDC, Fort
;      STREET:  Detrick
;      CITY:  Frederick
;      STATE:  MD
;      COUNTRY:  US
;      ZIP:  21702-5012
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/348,920
;      FILING DATE:  25-NOV-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  doc348,920
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 619-7807
;      TELEFAX:  301-619-7714
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  575 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
US-08-348-920-2

  Query Match             92.0%;  Score 80;  DB 1;  Length 575;
  Best Local Similarity   92.3%;  Pred. No. 0.002;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              |||||||||:|||
Db        548 EFHRWSSYMMHWK 560


RESULT 21
5200183-5
;Patent No. 5200183
;    APPLICANT: TANG, JORDAN J.N.;WANG, CHI-SUN
;    TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES
;    NUMBER OF SEQUENCES: 22
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/537,426
;      FILING DATE: 12-JUN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 504,635
;      FILING DATE: 04-APR-1990
;      APPLICATION NUMBER: 122,410
;      FILING DATE: 19-NOV-1987
;SEQ ID NO:5:
;      LENGTH: 572
5200183-5

  Query Match             71.3%;  Score 62;  DB 6;  Length 572;
  Best Local Similarity   64.3%;  Pred. No. 0.56;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        543 AGFHRWNNYMMDWK 556


RESULT 22
5200183-5
;Patent No. 5200183
;    APPLICANT: TANG, JORDAN J.N.;WANG, CHI-SUN
;    TITLE OF INVENTION: RECOMBINANT BILE SALT ACTIVATED LIPASES
;    NUMBER OF SEQUENCES: 22
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/537,426
;      FILING DATE: 12-JUN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 504,635
;      FILING DATE: 04-APR-1990
;      APPLICATION NUMBER: 122,410
;      FILING DATE: 19-NOV-1987
;SEQ ID NO:5:
;      LENGTH: 572
5200183-5

  Query Match             71.3%;  Score 62;  DB 6;  Length 572;
  Best Local Similarity   64.3%;  Pred. No. 0.56;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        543 AGFHRWNNYMMDWK 556


RESULT 23
5215909-12
;Patent No. 5215909
;    APPLICANT: SOREQ, HERMONA
;    TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
;    NUMBER OF SEQUENCES: 13
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/572,911
;      FILING DATE: 15-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 87,724
;      FILING DATE: 21-AUG-1987
;      APPLICATION NUMBER: 875,737
;      FILING DATE: 18-JUN-1986
;SEQ ID NO:12:
;      LENGTH: 573
5215909-12

  Query Match             71.3%;  Score 62;  DB 6;  Length 573;
  Best Local Similarity   64.3%;  Pred. No. 0.56;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        544 AGFHRWNNYMMDWK 557


RESULT 24
5215909-12
;Patent No. 5215909
;    APPLICANT: SOREQ, HERMONA
;    TITLE OF INVENTION: HUMAN CHOLINESTERASE GENES
;    NUMBER OF SEQUENCES: 13
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/572,911
;      FILING DATE: 15-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 87,724
;      FILING DATE: 21-AUG-1987
;      APPLICATION NUMBER: 875,737
;      FILING DATE: 18-JUN-1986
;SEQ ID NO:12:
;      LENGTH: 573
5215909-12

  Query Match             71.3%;  Score 62;  DB 6;  Length 573;
  Best Local Similarity   64.3%;  Pred. No. 0.56;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        544 AGFHRWNNYMMDWK 557


RESULT 25
US-08-446-100-1
; Sequence 1, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
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;      ORGANISM:  human esterases
US-08-446-100-1

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 26
US-08-446-100-2
; Sequence 2, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-2

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 27
US-08-446-100-3
; Sequence 3, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-3

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 28
US-08-446-100-4
; Sequence 4, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
```

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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-4

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 29
US-08-446-100-5
; Sequence 5, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-5

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 30
US-08-446-100-6
; Sequence 6, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-6

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586
```

```
RESULT 31
US-08-446-100-7
; Sequence 7, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-7

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 32
US-08-446-100-8
; Sequence 8, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-8

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 33
US-08-446-100-9
; Sequence 9, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  9:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-9

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 34
US-08-446-100-10
; Sequence 10, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-10

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 35
US-08-446-100-11
; Sequence 11, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-11

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 36
US-08-446-100-12
; Sequence 12, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
```

```
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-12

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 37
US-08-446-100-13
; Sequence 13, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-13

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 38
US-08-446-100-14
; Sequence 14, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-14
```

```
  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 39
US-08-446-100-15
; Sequence 15, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-15

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 40
US-08-446-100-16
; Sequence 16, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-16

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 41
US-08-446-100-17
; Sequence 17, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
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;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-17

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 42
US-08-446-100-18
; Sequence 18, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-18

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 43
US-08-446-100-24
; Sequence 24, Application US/08446100
; Patent No. 6001625
;  GENERAL INFORMATION:
;    APPLICANT:  Broomfield, Clarence A
;    APPLICANT:  Millard, Charles B
;    APPLICANT:  Lockridge, Oksana
;    TITLE OF INVENTION:  Site-Directed Mutagenesis of Esterases
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hendricks and Assoc.
;      STREET:  9669 A Main Street, P.O. Box 2509
;      CITY:  Fairfax
;      STATE:  VA
;      COUNTRY:  US
;      ZIP:  22031
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,100
;      FILING DATE:  19-MAY-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hendricks, Glenna
;      REGISTRATION NUMBER:  32,535
;      REFERENCE/DOCKET NUMBER:  broomfield
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 425-4250
;      TELEFAX:  (703) 425-2767
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  602 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  human esterases
US-08-446-100-24

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 44
US-09-334-489-3
```

```
; Sequence 3, Application US/09334489
; Patent No. 6291175
; GENERAL INFORMATION:
;  APPLICANT:  Pierre Sevigny
;  APPLICANT:  Keith Schappert
;  APPLICANT:  Heiko Wiesbusch
;  TITLE OF INVENTION:  METHODS FOR TREATING A NEUROLOGICAL
;  TITLE OF INVENTION:  DISEASE BY DETERMINING BCHE GENOTYPE
;  FILE REFERENCE:  08523/013002
;  CURRENT APPLICATION NUMBER: US/09/334,489
;  CURRENT FILING DATE:  1999-06-16
;  PRIOR APPLICATION NUMBER:  60/089,406
;  PRIOR FILING DATE:  1998-06-18
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 602
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-334-489-3

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 45
US-09-334-489-4
; Sequence 4, Application US/09334489
; Patent No. 6291175
; GENERAL INFORMATION:
;  APPLICANT:  Pierre Sevigny
;  APPLICANT:  Keith Schappert
;  APPLICANT:  Heiko Wiesbusch
;  TITLE OF INVENTION:  METHODS FOR TREATING A NEUROLOGICAL
;  TITLE OF INVENTION:  DISEASE BY DETERMINING BCHE GENOTYPE
;  FILE REFERENCE:  08523/013002
;  CURRENT APPLICATION NUMBER: US/09/334,489
;  CURRENT FILING DATE:  1999-06-16
;  PRIOR APPLICATION NUMBER:  60/089,406
;  PRIOR FILING DATE:  1998-06-18
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 602
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-334-489-4

  Query Match             71.3%;  Score 62;  DB 3;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.59;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


Search completed: October 12, 2005, 10:23:41
Job time : 46 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 12, 2005, 10:06:29 ; Search time 56 Seconds
(without alignments)
128.020 Million cell updates/sec

Title: US-09-155-076-1
Perfect score: 87
Sequence: 1 AEFHRWSSYMVHWK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	87	100.0	39	2	Q9TSJ6	Q9tsj6 bos taurus
2	87	100.0	526	2	Q86YX9	Q86yx9 homo sapien
3	87	100.0	584	1	ACES_RABIT	Q29499 oryctolagus
4	87	100.0	611	1	ACES_FELCA	O62763 felis silve
5	87	100.0	613	1	ACES_BOVIN	P23795 bos taurus
6	87	100.0	614	1	ACES_HUMAN	P22303 homo sapien
7	87	100.0	614	1	ACES_MOUSE	P21836 mus musculu
8	87	100.0	614	1	ACES_RAT	P37136 rattus norv
9	87	100.0	614	2	Q67BC1	Q67bc1 macaca mula
10	84	96.6	633	1	ACES_ELEEL	O42275 electrophor
11	80	92.0	95	2	Q9W6Y8	Q9w6y8 torpedo cal
12	80	92.0	634	1	ACES_BRARE	Q9dde3 brachydanio
13	70	80.5	606	1	ACES_BUNFA	Q92035 bungarus fa
14	65	74.7	597	2	Q9JKC1	Q9jkc1 rattus norv
15	65	74.7	767	1	ACES_CHICK	P36196 gallus gall
16	62	71.3	64	2	Q96HL2	Q96h12 homo sapien
17	62	71.3	574	1	CHLE_HORSE	P81908 equus cabal
18	62	71.3	602	1	CHLE_HUMAN	P06276 homo sapien
19	62	71.3	602	2	Q9N1N9	Q9n1n9 equus cabal
20	62	71.3	603	2	Q90ZK8	Q90zk8 gallus gall
21	61	70.1	581	1	CHLE_RABIT	P21927 oryctolagus
22	61	70.1	603	1	CHLE_MOUSE	Q03311 mus musculu
23	56	64.4	602	1	CHLE_FELCA	O62760 felis silve
24	56	64.4	602	1	CHLE_PANTT	O62761 panthera ti
25	48	55.2	205	2	Q8B0J7	Q8b0j7 california
26	47	54.0	550	2	Q7RTL7	Q7rtl7 ciona savig
27	46.5	53.4	667	2	Q64NA7	Q64na7 bacteroides
28	45	51.7	709	2	Q759Y3	Q759y3 ashbya goss
29	44	50.6	143	2	Q857V6	Q857v6 mycobacteri
30	44	50.6	260	2	O78318	O78318 arabidopsis
31	44	50.6	328	2	Q8HRN8	Q8hrn8 arabidopsis
32	44	50.6	357	2	Q6YT37	Q6yt37 sus scrofa
33	44	50.6	467	2	Q7S6U0	Q7s6u0 neurospora
34	44	50.6	746	1	NU5C_ARATH	P56752 arabidopsis
35	43.5	50.0	270	2	Q94BA9	Q94ba9 rhagodia ba
36	43.5	50.0	651	2	Q89Z67	Q89z67 bacteroides
37	43.5	50.0	692	2	Q8A059	Q8a059 bacteroides
38	43	49.4	186	2	Q7MZE7	Q7mze7 photorhabdu
39	43	49.4	196	2	Q853E9	Q853e9 mycobacteri
40	43	49.4	223	2	Q96BH3	Q96bh3 homo sapien
41	43	49.4	223	2	Q96RT0	Q96rt0 homo sapien
42	43	49.4	392	2	Q9LMW9	Q9lmw9 arabidopsis
43	43	49.4	422	2	Q9LM89	Q9lm89 arabidopsis
44	43	49.4	516	1	SMP3_YEAST	Q04174 saccharomyc
45	43	49.4	564	2	Q95TI1	Q95ti1 drosophila
46	43	49.4	593	2	Q9I7D7	Q9i7d7 drosophila
47	43	49.4	2070	2	Q8KLL3	Q8kll3 streptomyce
48	42	48.3	100	2	Q9ABN2	Q9abn2 caulobacter
49	42	48.3	116	2	Q8WBV7	Q8wbv7 ostrinia nu
50	42	48.3	117	2	Q8WB28	Q8wb28 ostrinia fu
51	42	48.3	138	2	Q8P935	Q8p935 xanthomonas
52	42	48.3	138	2	Q8PKN2	Q8pkn2 xanthomonas
53	42	48.3	143	2	Q8FRL6	Q8frl6 corynebacte
54	42	48.3	150	2	Q8PRG8	Q8prg8 xanthomonas
55	42	48.3	261	2	Q9GL26	Q9gl26 canis famil
56	42	48.3	322	2	Q6D6E9	Q6d6e9 erwinia car
57	42	48.3	553	2	Q7SX87	Q7sx87 brachydanio
58	42	48.3	558	2	Q99KQ8	Q99kq8 mus musculu
59	42	48.3	657	2	Q9UUQ3	Q9uuq3 orpinomyces
60	42	48.3	657	2	Q9GDW2	Q9gdw2 smilax hisp
61	42	48.3	664	2	Q9C122	Q9c122 piromyces s
62	42	48.3	723	2	Q89YE5	Q89ye5 bradyrhizob
63	42	48.3	755	2	Q659E9	Q659e9 homo sapien
64	42	48.3	768	2	Q64UC7	Q64uc7 bacteroides
65	42	48.3	822	1	ANC2_HUMAN	Q9ujx6 homo sapien
66	42	48.3	837	1	ANC2_MOUSE	Q8bzq7 mus musculu
67	42	48.3	838	2	Q6ZPR8	Q6zpr8 mus musculu
68	42	48.3	1084	2	Q9H1R7	Q9h1r7 homo sapien
69	42	48.3	1103	2	Q7TMJ2	Q7tmj2 mus musculu
70	42	48.3	1788	2	O60611	O60611 homo sapien
71	42	48.3	1788	2	O60612	O60612 homo sapien
72	42	48.3	1792	2	O46385	O46385 bos taurus
73	42	48.3	2031	2	Q8K4L2	Q8k412 mus musculu
74	42	48.3	2073	2	Q6U1J6	Q6u1j6 mustela put
75	42	48.3	2170	2	Q8K4L3	Q8k413 mus musculu
76	42	48.3	2214	2	O95425	O95425 homo sapien
77	41.5	47.7	133	2	Q6D801	Q6d801 erwinia car
78	41	47.1	117	2	Q94XC9	Q94xc9 caecilius q
79	41	47.1	145	2	Q675X0	Q675x0 oikopleura
80	41	47.1	153	2	Q98HQ0	Q98hq0 rhizobium l
81	41	47.1	177	2	Q9RMA7	Q9rma7 bacillus ci
82	41	47.1	220	2	Q9NWQ6	Q9nwq6 homo sapien
83	41	47.1	230	2	Q8GVB4	Q8gvb4 leucojum ae
84	41	47.1	237	2	Q62GB7	Q62gb7 burkholderi
85	41	47.1	237	2	Q63Q65	Q63q65 burkholderi
86	41	47.1	242	2	Q8GVA9	Q8gva9 acis nicaee
87	41	47.1	250	2	Q8GVA4	Q8gva4 acis valent
88	41	47.1	250	2	Q8GVB3	Q8gvb3 acis autumn
89	41	47.1	289	2	Q6MLZ2	Q6mlz2 bdellovibri
90	41	47.1	290	2	Q97MU8	Q97mu8 clostridium
91	41	47.1	336	2	Q7NAA3	Q7naa3 photorhabdu
92	41	47.1	368	2	Q8A4F2	Q8a4f2 bacteroides
93	41	47.1	378	2	Q9TMJ8	Q9tmj8 leucojum ae
94	41	47.1	378	2	Q9TMK2	Q9tmk2 galanthus e
95	41	47.1	397	2	Q9V095	Q9v095 pyrococcus
96	41	47.1	398	2	Q986I8	Q986i8 rhizobium l
97	41	47.1	408	2	Q8TH21	Q8th21 pyrococcus
98	41	47.1	414	2	Q9UM44	Q9um44 homo sapien
99	41	47.1	468	2	Q8R157	Q8r157 mus musculu
100	41	47.1	477	2	Q8M904	Q8m904 stylidium b
101	41	47.1	499	2	Q8DHN3	Q8dhn3 synechococc
102	41	47.1	509	2	Q9FNY9	Q9fny9 arabidopsis
103	41	47.1	512	2	Q9C8X2	Q9c8x2 arabidopsis
104	41	47.1	516	2	Q8GV94	Q8gv94 galanthus n

105	41	47.1	520	2	Q8GV99	Q8gv99	galanthus f
106	41	47.1	520	2	Q8GVA0	Q8gva0	galanthus e
107	41	47.1	520	2	Q8GVA1	Q8gva1	galanthus c
108	41	47.1	520	2	Q8GVA2	Q8gva2	galanthus a
109	41	47.1	520	2	Q8GVA5	Q8gva5	acis valent
110	41	47.1	520	2	Q8GVB2	Q8gvb2	acis autumn
111	41	47.1	520	2	Q8GVB5	Q8gvb5	leucojum ae
112	41	47.1	523	2	Q97GW8	Q97gw8	clostridium
113	41	47.1	527	2	Q8GDM1	Q8gdm1	photorhabdu
114	41	47.1	535	2	Q9KAJ7	Q9kaj7	bacillus ha
115	41	47.1	694	2	Q7SEV8	Q7sev8	neurospora
116	41	47.1	818	2	Q9KB88	Q9kb88	bacillus ha
117	41	47.1	1155	2	Q6TKT8	Q6tkt8	escherichia
118	41	47.1	1181	2	Q8GDN1	Q8gdn1	photorhabdu
119	41	47.1	1243	2	Q6GQT8	Q6gqt8	mus musculu
120	41	47.1	1252	2	Q9BLU9	Q9blu9	leishmania
121	41	47.1	1261	2	Q90ZW5	Q90zw5	gallus gall
122	41	47.1	1323	1	SAL3_MOUSE	Q62255	mus musculu
123	41	47.1	1687	2	Q7F8R6	Q7f8r6	oryza sativ
124	41	47.1	2803	2	Q748V3	Q748v3	geobacter s
125	40.5	46.6	160	2	Q834W9	Q834w9	enterococcu
126	40.5	46.6	175	2	Q6BS90	Q6bs90	debaryomyce
127	40.5	46.6	212	2	Q6BS89	Q6bs89	debaryomyce
128	40.5	46.6	265	2	Q94BB9	Q94bb9	plinthus cr
129	40.5	46.6	269	2	Q719D8	Q719d8	silene nuta
130	40.5	46.6	269	2	Q94B96	Q94b96	silene roth
131	40.5	46.6	270	2	Q94BB5	Q94bb5	portulacari
132	40.5	46.6	271	2	Q94BG3	Q94bg3	galenia pub
133	40.5	46.6	274	2	Q94BK1	Q94bk1	axyris hybr
134	40.5	46.6	276	2	Q94BF0	Q94bf0	honckenya p
135	40.5	46.6	277	2	Q94BF3	Q94bf3	halophytum
136	40.5	46.6	277	2	Q94BL4	Q94bl4	agdestis cl
137	40.5	46.6	278	2	Q94BL9	Q94bl9	achatocarpu
138	40.5	46.6	280	2	Q94BC1	Q94bc1	phytolacca
139	40.5	46.6	280	2	Q94BH6	Q94bh6	didierea tr
140	40.5	46.6	281	2	Q94BC0	Q94bc0	pisonia umb
141	40.5	46.6	281	2	Q94BC8	Q94bc8	oxybaphus n
142	40.5	46.6	281	2	Q94BH8	Q94bh8	decarya mad
143	40.5	46.6	283	2	Q94BL1	Q94bl1	alluaudia a
144	40.5	46.6	285	2	Q94BC2	Q94bc2	phaulothamn
145	40.5	46.6	285	2	Q94BI9	Q94bi9	calyptrothe
146	40.5	46.6	289	2	Q94BF9	Q94bf9	glischrotha
147	40.5	46.6	293	2	Q94BL0	Q94bl0	alluaudiops
148	40.5	46.6	442	2	Q9L1F1	Q9l1f1	streptomyce
149	40.5	46.6	469	2	Q7NX74	Q7nx74	chromobacte
150	40.5	46.6	502	2	Q98DL0	Q98dl0	rhizobium l
151	40.5	46.6	508	2	O78332	O78332	pergularia
152	40.5	46.6	510	1	ACO1_YEAST	P21147	saccharomyc
153	40.5	46.6	510	2	Q6B1S0	Q6b1s0	saccharomyc
154	40.5	46.6	511	2	O78334	O78334	tylophora i
155	40.5	46.6	511	2	O78335	O78335	vincetoxicu
156	40.5	46.6	1052	2	Q7QBI2	Q7qbi2	anopheles g
157	40	46.0	67	2	Q8EEE0	Q8eee0	shewanella
158	40	46.0	136	2	Q6YYF6	Q6yyf6	oryza sativ
159	40	46.0	183	2	Q57000	Q57000	zymomonas m
160	40	46.0	211	2	Q9K8C4	Q9k8c4	bacillus ha
161	40	46.0	218	2	Q8GV90	Q8gv90	galanthus r
162	40	46.0	232	2	Q8GVA8	Q8gva8	acis rosea.
163	40	46.0	243	2	Q8W5L5	Q8w5l5	oryza sativ
164	40	46.0	243	2	Q7XH69	Q7xh69	oryza sativ
165	40	46.0	245	1	YG24_YEAST	P53237	saccharomyc
166	40	46.0	249	1	UBIE_LEPIN	Q8exj3	leptospira
167	40	46.0	249	2	Q75FL1	Q75fl1	leptospira
168	40	46.0	268	2	Q94BI3	Q94bi3	claytonia m
169	40	46.0	271	2	Q94BF1	Q94bf1	hilleria la
170	40	46.0	274	2	Q94B98	Q94b98	seguieria a
171	40	46.0	283	2	Q94BD6	Q94bd6	montia parv
172	40	46.0	303	2	Q82RI8	Q82ri8	streptomyce
173	40	46.0	314	2	Q7PVC6	Q7pvc6	anopheles g
174	40	46.0	330	2	Q8HRS0	Q8hrs0	cadaba virg
175	40	46.0	330	2	Q8HRS1	Q8hrs1	cadaba kirk
176	40	46.0	351	2	O72754	O72754	cowpox viru
177	40	46.0	355	2	Q87H15	Q87h15	vibrio para
178	40	46.0	378	2	Q9TMG2	Q9tmg2	crocus sati
179	40	46.0	450	2	O25000	O25000	helicobacte
180	40	46.0	453	2	Q6UVW8	Q6uvw8	homo sapien
181	40	46.0	517	2	Q9XPP6	Q9xpp6	pseudotrill
182	40	46.0	520	2	Q8GV95	Q8gv95	galanthus l
183	40	46.0	521	2	Q877D5	Q877d5	pyrobaculum
184	40	46.0	534	2	Q7ZWN9	Q7zwn9	xenopus lae
185	40	46.0	540	2	Q870B7	Q870b7	piromyces s
186	40	46.0	586	2	Q74IP7	Q74ip7	lactobacill
187	40	46.0	606	2	Q8REH6	Q8reh6	fusobacteri
188	40	46.0	650	2	Q7RZT5	Q7rzt5	neurospora
189	40	46.0	658	2	Q9GDW8	Q9gdw8	androcymbiu
190	40	46.0	665	2	Q870B6	Q870b6	piromyces s
191	40	46.0	678	2	Q716T9	Q716t9	kreysigia s
192	40	46.0	690	2	Q6UVW7	Q6uvw7	homo sapien
193	40	46.0	707	2	Q8NEE6	Q8nee6	homo sapien
194	40	46.0	716	1	RRP2_IAHTE	P13169	influenza a
195	40	46.0	731	2	Q6TMX8	Q6tmx8	schistosoma
196	40	46.0	735	2	Q8N7Y4	Q8n7y4	homo sapien
197	40	46.0	736	2	Q6TMY2	Q6tmy2	schistosoma
198	40	46.0	740	2	Q6TMY0	Q6tmy0	schistosoma
199	40	46.0	749	2	Q7V511	Q7v511	prochloroco
200	40	46.0	773	2	Q8IG87	Q8ig87	drosophila
201	40	46.0	844	2	Q8S9X1	Q8s9x1	oryza sativ
202	40	46.0	1179	2	Q9N8M4	Q9n8m4	trypanosoma
203	40	46.0	1350	2	Q91929	Q91929	xenopus lae
204	40	46.0	1784	2	Q9VE54	Q9ve54	drosophila
205	40	46.0	1995	1	YCX7_CHLRE	P36495	chlamydomon
206	39.5	45.4	198	2	Q7NDG5	Q7ndg5	gloeobacter
207	39.5	45.4	276	2	Q6R1V7	Q6r1v7	sapranthus
208	39.5	45.4	276	2	Q6R1X1	Q6r1x1	polyalthia
209	39.5	45.4	276	2	Q6R1X2	Q6r1x2	polyalthia
210	39.5	45.4	276	2	Q6R1X3	Q6r1x3	polyalthia
211	39.5	45.4	276	2	Q6R1X4	Q6r1x4	enicosanthu
212	39.5	45.4	276	2	Q6R1X6	Q6r1x6	enicosanthu
213	39.5	45.4	276	2	Q6R1X7	Q6r1x7	polyalthia
214	39.5	45.4	276	2	Q6R1X8	Q6r1x8	polyalthia
215	39.5	45.4	276	2	Q6R1X9	Q6r1x9	polyalthia
216	39.5	45.4	276	2	Q6R1Y0	Q6r1y0	polyalthia
217	39.5	45.4	276	2	Q6R1Y1	Q6r1y1	polyalthia
218	39.5	45.4	276	2	Q6R1Y2	Q6r1y2	polyalthia
219	39.5	45.4	429	2	Q9GG33	Q9gg33	limnobium l
220	39.5	45.4	435	2	Q9GG34	Q9gg34	lagarosipho
221	39.5	45.4	440	2	Q7Z4R4	Q7z4r4	homo sapien
222	39.5	45.4	447	2	Q6ZMD5	Q6zmd5	homo sapien
223	39.5	45.4	469	2	P73738	P73738	synechocyst
224	39.5	45.4	470	2	Q6GDT2	Q6gdt2	staphylococ
225	39.5	45.4	494	2	Q7UB36	Q7ub36	shigella fl
226	39.5	45.4	497	2	Q83PI3	Q83pi3	shigella fl
227	39.5	45.4	498	2	Q6CZD8	Q6czd8	erwinia car
228	39.5	45.4	507	2	Q717Z2	Q717z2	annona muri
229	39.5	45.4	509	2	Q7YKL8	Q7ykl8	genlisea ro
230	39.5	45.4	510	2	Q7YKM1	Q7ykm1	genlisea au
231	39.5	45.4	512	2	O78333	O78333	pentarrhinu
232	39.5	45.4	542	2	O64858	O64858	arabidopsis
233	39.5	45.4	611	2	Q96PB9	Q96pb9	homo sapien
234	39.5	45.4	611	2	Q9H068	Q9h068	homo sapien
235	39.5	45.4	618	2	Q96GS7	Q96gs7	homo sapien
236	39.5	45.4	618	2	Q9H6U8	Q9h6u8	homo sapien
237	39.5	45.4	699	2	Q9P9J5	Q9p9j5	sulfolobus
238	39.5	45.4	1057	2	Q9Y8H1	Q9y8h1	tricholoma
239	39.5	45.4	1198	2	Q6FPG4	Q6fpg4	candida gla
240	39	44.8	48	2	Q85KI0	Q85ki0	trissolcus
241	39	44.8	100	2	O23949	O23949	gossypium h
242	39	44.8	116	2	Q8SEY7	Q8sey7	bombyx mand
243	39	44.8	116	2	Q9MIE8	Q9mie8	bombyx mori
244	39	44.8	118	2	Q6JVA0	Q6jva0	bombyx mand
245	39	44.8	138	1	HV48_MOUSE	P03980	mus musculu
246	39	44.8	143	2	Q69SG2	Q69sg2	oryza sativ
247	39	44.8	150	2	Q6YBA2	Q6yba2	staphylococ
248	39	44.8	150	2	Q6YBA3	Q6yba3	staphylococ
249	39	44.8	150	2	Q6YBA4	Q6yba4	staphylococ
250	39	44.8	150	2	Q6YBA6	Q6yba6	staphylococ

251	39	44.8	150	2	Q6YBA8	Q6yba8	staphylococ
252	39	44.8	150	2	Q6YBB0	Q6ybb0	staphylococ
253	39	44.8	151	2	Q8NSG0	Q8nsg0	corynebacte
254	39	44.8	155	2	Q9K2H1	Q9k2h1	staphylococ
255	39	44.8	155	2	Q9K2M4	Q9k2m4	staphylococ
256	39	44.8	155	2	Q9L3Y9	Q9l3y9	staphylococ
257	39	44.8	155	2	Q9L3Z0	Q9l3z0	staphylococ
258	39	44.8	155	2	Q9L3Z1	Q9l3z1	staphylococ
259	39	44.8	155	2	Q9L3Z2	Q9l3z2	staphylococ
260	39	44.8	157	2	Q84B73	Q84b73	vibrio natr
261	39	44.8	157	2	Q8GFH1	Q8gfh1	vibrio pela
262	39	44.8	157	2	Q87NK2	Q87nk2	vibrio para
263	39	44.8	166	2	Q8D5M2	Q8d5m2	vibrio vuln
264	39	44.8	168	2	Q6FBI6	Q6fbi6	acinetobact
265	39	44.8	170	2	Q7V9Z1	Q7v9z1	prochloroco
266	39	44.8	199	2	Q9KUL9	Q9kul9	vibrio chol
267	39	44.8	213	2	Q7RZ07	Q7rz07	neurospora
268	39	44.8	223	2	Q871E2	Q871e2	neurospora
269	39	44.8	226	1	VME1_PEDV7	P59771	porcine epi
270	39	44.8	226	1	VME1_PEDVB	P59770	porcine epi
271	39	44.8	226	2	O37049	O37049	porcine epi
272	39	44.8	226	2	O37351	O37351	porcine epi
273	39	44.8	226	2	O72839	O72839	porcine epi
274	39	44.8	226	2	Q91AU9	Q91au9	porcine epi
275	39	44.8	226	2	Q692M0	Q692m0	porcine epi
276	39	44.8	226	2	Q6J0S8	Q6j0s8	porcine epi
277	39	44.8	230	2	Q91EZ1	Q91ez1	cydia pomon
278	39	44.8	240	2	Q81IR5	Q81ir5	bacillus ce
279	39	44.8	259	2	O78312	O78312	sisymbrium
280	39	44.8	260	2	O78311	O78311	brassica ol
281	39	44.8	260	2	O78319	O78319	stanleya pi
282	39	44.8	260	2	O78320	O78320	thlaspi arv
283	39	44.8	262	2	O10441	O10441	mouse adeno
284	39	44.8	266	2	Q93HH2	Q93hh2	streptomyce
285	39	44.8	272	2	Q99UH4	Q99uh4	staphylococ
286	39	44.8	272	2	Q7A106	Q7a106	staphylococ
287	39	44.8	272	2	Q7A5V8	Q7a5v8	staphylococ
288	39	44.8	272	2	Q6G9R4	Q6g9r4	staphylococ
289	39	44.8	272	2	Q6GHD6	Q6ghd6	staphylococ
290	39	44.8	274	2	Q896N4	Q896n4	clostridium
291	39	44.8	274	2	Q8CPE7	Q8cpe7	staphylococ
292	39	44.8	277	2	Q9FYE3	Q9fye3	arabidopsis
293	39	44.8	280	2	Q94BL3	Q94bl3	agrostemma
294	39	44.8	298	2	Q7SXV5	Q7sxv5	brachydanio
295	39	44.8	299	2	Q67VG2	Q67vg2	oryza sativ
296	39	44.8	299	2	Q6ANJ8	Q6anj8	desulfotale
297	39	44.8	308	2	Q7XDX0	Q7xdx0	oryza sativ
298	39	44.8	318	2	Q6A7W9	Q6a7w9	propionibac
299	39	44.8	328	2	Q8HRN1	Q8hrn1	stanleya pi
300	39	44.8	328	2	Q8HRN2	Q8hrn2	sisymbrium
301	39	44.8	335	2	Q9L6I0	Q9l6i0	thiocapsa r
302	39	44.8	342	2	Q719H0	Q719h0	triglochin
303	39	44.8	357	2	Q6N2K6	Q6n2k6	rhodopseudo
304	39	44.8	357	2	Q89HM5	Q89hm5	bradyrhizob
305	39	44.8	374	2	Q654H0	Q654h0	oryza sativ
306	39	44.8	376	2	Q6Q2L1	Q6q2l1	hyposoter f
307	39	44.8	394	2	Q8A2D1	Q8a2d1	bacteroides
308	39	44.8	400	2	Q67VG3	Q67vg3	oryza sativ
309	39	44.8	401	2	Q8RUP6	Q8rup6	oryza sativ
310	39	44.8	408	2	Q9HXZ9	Q9hxz9	pseudomonas
311	39	44.8	422	2	Q8EH43	Q8eh43	shewanella
312	39	44.8	441	2	O15814	O15814	dictyosteli
313	39	44.8	444	2	Q8PF64	Q8pf64	xanthomonas
314	39	44.8	451	2	Q7QL14	Q7ql14	anopheles g
315	39	44.8	498	2	Q6LA25	Q6la25	triglochin
316	39	44.8	500	2	Q7Y1V8	Q7y1v8	zostera cae
317	39	44.8	506	2	Q9GHB4	Q9ghb4	freycinetia
318	39	44.8	507	1	SXA2_SCHPO	P32825	schizosacch
319	39	44.8	513	2	Q7XC43	Q7xc43	oryza sativ
320	39	44.8	513	2	Q9AY56	Q9ay56	oryza sativ
321	39	44.8	524	2	O49650	O49650	arabidopsis
322	39	44.8	524	2	Q93ZX2	Q93zx2	arabidopsis
323	39	44.8	526	2	O49652	O49652	arabidopsis
324	39	44.8	542	2	Q7TPQ2	Q7tpq2	mus musculu
325	39	44.8	575	1	UL87_EBV	P25215	epstein-bar
326	39	44.8	644	1	PSAB_AMPCA	P58383	amphidinium
327	39	44.8	651	2	Q8NYB1	Q8nyb1	staphylococ
328	39	44.8	651	2	Q932J5	Q932j5	staphylococ
329	39	44.8	651	2	Q99WP4	Q99wp4	staphylococ
330	39	44.8	651	2	Q6GCD9	Q6gcd9	staphylococ
331	39	44.8	651	2	Q6GJY4	Q6gjy4	staphylococ
332	39	44.8	654	2	Q70G41	Q70g41	amphidinium
333	39	44.8	656	2	Q9GDX8	Q9gdx8	clintonia b
334	39	44.8	660	2	Q9GDX1	Q9gdx1	notholirion
335	39	44.8	667	2	Q7UM38	Q7um38	rhodopirell
336	39	44.8	690	2	Q6EMT9	Q6emt9	marantochlo
337	39	44.8	750	2	Q8AZJ6	Q8azj6	human herpe
338	39	44.8	866	2	Q6UEQ7	Q6ueq7	human immun
339	39	44.8	945	2	Q6CYB0	Q6cyb0	kluyveromyc
340	39	44.8	1060	2	Q7UKA3	Q7uka3	rhodopirell
341	39	44.8	1237	1	YDY2_SCHPO	O13683	schizosacch
342	39	44.8	1300	1	SAL3_HUMAN	Q9bxa9	homo sapien
343	39	44.8	1368	2	Q9N531	Q9n531	caenorhabdi
344	39	44.8	1401	2	Q9N530	Q9n530	caenorhabdi
345	39	44.8	1679	2	Q7Q7K8	Q7q7k8	anopheles g
346	38.5	44.3	177	2	Q7Q782	Q7q782	anopheles g
347	38.5	44.3	185	2	Q7PDX1	Q7pdx1	anopheles g
348	38.5	44.3	196	2	Q8YQY7	Q8yqy7	anabaena sp
349	38.5	44.3	204	2	Q82NS6	Q82ns6	streptomyce
350	38.5	44.3	269	2	Q8WI39	Q8wi39	dioscorea c
351	38.5	44.3	270	2	Q8CQ43	Q8cq43	staphylococ
352	38.5	44.3	275	2	Q94BJ3	Q94bj3	bosea cypri
353	38.5	44.3	277	2	Q932F3	Q932f3	staphylococ
354	38.5	44.3	277	2	Q99VX8	Q99vx8	staphylococ
355	38.5	44.3	277	2	Q7A1M3	Q7a1m3	staphylococ
356	38.5	44.3	277	2	Q6GBJ2	Q6gbj2	staphylococ
357	38.5	44.3	277	2	Q6GJ32	Q6gj32	staphylococ
358	38.5	44.3	280	2	Q94BB4	Q94bb4	psilotrichu
359	38.5	44.3	283	2	Q94BD7	Q94bd7	moehringia
360	38.5	44.3	287	1	XT14_ARATH	Q9zsu4	arabidopsis
361	38.5	44.3	354	2	O98848	O98848	cornus cana
362	38.5	44.3	495	2	Q7UXA8	Q7uxa8	rhodopirell
363	38.5	44.3	499	2	Q9CJZ0	Q9cjz0	pasteurella
364	38.5	44.3	517	2	Q9GHB5	Q9ghb5	dioscorea a
365	38.5	44.3	613	2	Q940E7	Q940e7	agastache r
366	38.5	44.3	620	2	Q9FUW5	Q9fuw5	schizonepet
367	38.5	44.3	907	2	Q8YZ60	Q8yz60	anabaena sp
368	38	43.7	35	2	Q8SG47	Q8sg47	gasterophil
369	38	43.7	43	2	Q8SG43	Q8sg43	cf. senosto
370	38	43.7	50	2	Q8SG61	Q8sg61	ectinorhync
371	38	43.7	56	2	Q98928	Q98928	gallus gall
372	38	43.7	82	2	Q6B854	Q6b854	meriones un
373	38	43.7	117	1	NU3M_DROME	P18930	drosophila
374	38	43.7	117	1	NU3M_DROSU	P51940	drosophila
375	38	43.7	117	1	NU3M_DROYA	P07705	drosophila
376	38	43.7	117	2	Q6XSL5	Q6xsl5	bactrocera
377	38	43.7	117	2	Q7IV53	Q7iv53	drosophila
378	38	43.7	117	2	Q9MD67	Q9md67	drosophila
379	38	43.7	117	2	Q9MDN9	Q9mdn9	drosophila
380	38	43.7	117	2	Q9MGL2	Q9mgl2	drosophila
381	38	43.7	117	2	Q9MGL9	Q9mgl9	drosophila
382	38	43.7	117	2	Q9MGM8	Q9mgm8	drosophila
383	38	43.7	117	2	Q9XMN6	Q9xmn6	ceratitis c
384	38	43.7	118	2	Q9B2J0	Q9b2j0	chrysomya p
385	38	43.7	118	2	Q9MFP4	Q9mfp4	cochliomyia
386	38	43.7	137	2	Q71IR9	Q71ir9	lactobacill
387	38	43.7	157	2	Q9KSE7	Q9kse7	vibrio chol
388	38	43.7	162	2	Q7Q8F5	Q7q8f5	anopheles g
389	38	43.7	181	2	Q64AE2	Q64ae2	uncultured
390	38	43.7	181	2	Q64DV1	Q64dv1	uncultured
391	38	43.7	184	2	Q648T9	Q648t9	uncultured
392	38	43.7	184	2	Q64AW6	Q64aw6	uncultured
393	38	43.7	193	1	NADD_BRAJA	Q89x84	bradyrhizob
394	38	43.7	203	2	Q9U0N3	Q9u0n3	plasmodium
395	38	43.7	209	2	Q6NDE3	Q6nde3	rhodopseudo
396	38	43.7	210	2	Q6VF40	Q6vf40	pipa parva

397	38	43.7	218	2	Q7Q1X8	Q7q1x8	anopheles g
398	38	43.7	234	2	Q6J345	Q6j345	vaccinia vi
399	38	43.7	237	2	Q97UG9	Q97ug9	sulfolobus
400	38	43.7	239	2	Q7VJ29	Q7vj29	helicobacte
401	38	43.7	239	2	Q8UJ27	Q8uj27	agrobacteri
402	38	43.7	240	2	Q9VR89	Q9vr89	drosophila
403	38	43.7	245	2	Q9GL25	Q9gl25	canis famil
404	38	43.7	247	2	Q88EQ6	Q88eq6	pseudomonas
405	38	43.7	250	2	Q73TH3	Q73th3	mycobacteri
406	38	43.7	255	2	Q8XP77	Q8xp77	clostridium
407	38	43.7	265	2	Q7Q1X7	Q7q1x7	anopheles g
408	38	43.7	265	2	Q9DUN2	Q9dun2	vaccinia vi
409	38	43.7	267	1	TI32_ARATH	O22588	arabidopsis
410	38	43.7	279	2	Q675A4	Q675a4	physcomitre
411	38	43.7	280	2	Q8I5Q4	Q8i5q4	plasmodium
412	38	43.7	283	2	Q6FMX7	Q6fmx7	candida gla
413	38	43.7	286	2	Q67PH1	Q67ph1	symbiobacte
414	38	43.7	292	2	O97737	O97737	bos taurus
415	38	43.7	295	1	Y770_MYCTU	P71825	mycobacteri
416	38	43.7	295	2	Q7U1B4	Q7u1b4	mycobacteri
417	38	43.7	298	2	Q8Z8J2	Q8z8j2	salmonella
418	38	43.7	298	2	Q8ZR14	Q8zr14	salmonella
419	38	43.7	302	2	Q92YK3	Q92yk3	rhizobium m
420	38	43.7	313	2	Q8PUV7	Q8puv7	methanosarc
421	38	43.7	314	2	Q97AD4	Q97ad4	thermoplasm
422	38	43.7	315	2	Q9IFU7	Q9ifu7	bean 58058
423	38	43.7	321	2	Q63XT9	Q63xt9	burkholderi
424	38	43.7	324	2	Q654H2	Q654h2	oryza sativ
425	38	43.7	324	2	Q9JJS4	Q9jjs4	rattus norv
426	38	43.7	340	2	Q7V0U9	Q7v0u9	prochloroco
427	38	43.7	342	2	Q96I05	Q96i05	homo sapien
428	38	43.7	351	1	VB19_VACCD	P23998	vaccinia vi
429	38	43.7	351	1	VB19_VACCV	P25213	vaccinia vi
430	38	43.7	351	2	Q6RZB2	Q6rzb2	rabbitpox v
431	38	43.7	351	2	Q76ZK5	Q76zk5	vaccinia vi
432	38	43.7	352	2	Q8V4R2	Q8v4r2	monkeypox v
433	38	43.7	353	1	VB19_VACCC	P21077	vaccinia vi
434	38	43.7	353	2	Q6RFI1	Q6rfi1	vaccinia vi
435	38	43.7	353	2	Q9JF34	Q9jf34	vaccinia vi
436	38	43.7	355	2	Q6RFI2	Q6rfi2	cantagalo o
437	38	43.7	356	2	Q8WKY7	Q8wky7	arctostaphy
438	38	43.7	358	2	Q928M1	Q928m1	listeria in
439	38	43.7	364	2	Q9FYZ9	Q9fyz9	antirrhinum
440	38	43.7	366	2	Q8QMN5	Q8qmn5	cowpox viru
441	38	43.7	379	2	O44791	O44791	caenorhabdi
442	38	43.7	379	2	Q9TMI1	Q9tmi1	agapanthus
443	38	43.7	380	2	Q8DDT8	Q8ddt8	vibrio vuln
444	38	43.7	388	2	Q8LSQ2	Q8lsq2	oryza sativ
445	38	43.7	399	2	Q7MPY8	Q7mpy8	vibrio vuln
446	38	43.7	413	2	Q8NBB7	Q8nbb7	homo sapien
447	38	43.7	419	2	Q72E86	Q72e86	desulfovibr
448	38	43.7	422	2	Q9IMS8	Q9ims8	cherry mott
449	38	43.7	455	2	Q7MMJ4	Q7mmj4	vibrio vuln
450	38	43.7	455	2	Q8DG01	Q8dg01	vibrio vuln
451	38	43.7	468	2	Q880W3	Q880w3	pseudomonas
452	38	43.7	474	2	P93717	P93717	petunia hyb
453	38	43.7	478	2	Q8W3P8	Q8w3p8	phaseolus a
454	38	43.7	497	2	Q62BJ2	Q62bj2	burkholderi
455	38	43.7	497	2	Q63LV1	Q63lv1	burkholderi
456	38	43.7	511	2	Q9GHG8	Q9ghg8	acorus gram
457	38	43.7	515	1	MATK_TRIUN	Q9xpp8	trillium un
458	38	43.7	518	2	Q9TN83	Q9tn83	asparagus f
459	38	43.7	518	2	Q9TN84	Q9tn84	asparagus c
460	38	43.7	531	2	Q920A8	Q920a8	mus musculu
461	38	43.7	532	2	Q6P9J3	Q6p9j3	mus musculu
462	38	43.7	534	2	Q96PK1	Q96pk1	homo sapien
463	38	43.7	534	2	Q6P1U2	Q6p1u2	xenopus tro
464	38	43.7	536	2	Q9BSA4	Q9bsa4	homo sapien
465	38	43.7	551	2	Q89EZ3	Q89ez3	bradyrhizob
466	38	43.7	572	2	Q7NVS7	Q7nvs7	chromobacte
467	38	43.7	584	2	Q74IP6	Q74ip6	lactobacill
468	38	43.7	588	2	Q8VPI8	Q8vpi8	lactobacill
469	38	43.7	591	2	Q9KLQ4	Q9klq4	vibrio chol
470	38	43.7	601	2	Q6FK29	Q6fk29	candida gla
471	38	43.7	612	2	Q9HU20	Q9hu20	pseudomonas
472	38	43.7	616	2	Q64P12	Q64p12	bacteroides
473	38	43.7	619	2	Q9A2R4	Q9a2r4	caulobacter
474	38	43.7	645	2	Q67UQ9	Q67uq9	oryza sativ
475	38	43.7	650	2	Q42722	Q42722	daucus caro
476	38	43.7	657	2	Q9GDW0	Q9gdw0	streptopus
477	38	43.7	657	2	Q9GDW1	Q9gdw1	streptopus
478	38	43.7	657	2	Q9GDW5	Q9gdw5	prosartes m
479	38	43.7	660	2	Q9GDW3	Q9gdw3	scoliopus b
480	38	43.7	671	2	Q75HR4	Q75hr4	oryza sativ
481	38	43.7	672	2	Q95AT4	Q95at4	areca vesti
482	38	43.7	694	2	Q95AQ6	Q95aq6	beccariopho
483	38	43.7	698	2	Q95AS3	Q95as3	wettinia hi
484	38	43.7	703	2	Q6LFD2	Q6lfd2	plasmodium
485	38	43.7	710	2	Q87DS8	Q87ds8	xylella fas
486	38	43.7	710	2	Q9PDL6	Q9pdl6	xylella fas
487	38	43.7	727	1	DOC7_MOUSE	Q8r1a4	mus musculu
488	38	43.7	732	2	O61565	O61565	crassostrea
489	38	43.7	745	2	Q63TM1	Q63tm1	burkholderi
490	38	43.7	760	2	Q8J1E2	Q8j1e2	piromyces e
491	38	43.7	772	2	Q8XYD2	Q8xyd2	ralstonia s
492	38	43.7	788	2	Q9VGL9	Q9vgl9	drosophila
493	38	43.7	835	2	Q6FUJ7	Q6fuj7	candida gla
494	38	43.7	839	2	Q6PJ17	Q6pj17	mus musculu
495	38	43.7	846	2	Q6BSQ7	Q6bsq7	debaryomyce
496	38	43.7	864	2	O68395	O68395	thauera aro
497	38	43.7	864	2	Q8L1A3	Q8l1a3	thauera sp.
498	38	43.7	921	2	Q7SFM0	Q7sfm0	neurospora
499	38	43.7	928	2	Q6ZC53	Q6zc53	oryza sativ
500	38	43.7	1132	2	Q7NAF6	Q7naf6	mycoplasma

ALIGNMENTS

RESULT 1
Q9TSJ6
ID Q9TSJ6 PRELIMINARY; PRT; 39 AA.
AC Q9TSJ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Acetylcholinesterase T-subunit (Fragment).
GN Name=AChE;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98359754; PubMed=9693127;
RA Mendelson I., Kronman C., Ariel N., Shafferman A., Velan B.;
RT "Bovine acetylcholinesterase: cloning, expression and
RT characterization.";
RL Biochem. J. 334:251-259(1998).
DR EMBL; AF061816; AAC64269.1; -.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4959 MW; 72F3379D0F8B6557 CRC64;

Query Match 100.0%; Score 87; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
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Db 11 AEFHRWSSYMVHWK 24

RESULT 2

```
Q86YX9
ID   Q86YX9      PRELIMINARY;      PRT;   526 AA.
AC   Q86YX9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Apoptosis-related acetylcholinesterase (EC 3.1.1.7).
GN   Name=ARACHE;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yang L., Zhang X.J.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR   EMBL; AF334270; AAO32948.1; -.
DR   HSSP; P22303; 1F8U.
DR   GO; GO:0003990; F:acetylcholinesterase activity; IEA.
DR   GO; GO:0004104; F:cholinesterase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase.
SQ   SEQUENCE   526 AA;  58352 MW;  FB85F41EDFFF39DB CRC64;

  Query Match             100.0%;  Score 87;  DB 2;  Length 526;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        498 AEFHRWSSYMVHWK 511


RESULT 3
ACES_RABIT
ID   ACES_RABIT     STANDARD;      PRT;   584 AA.
AC   Q29499;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE) (Fragment).
GN   Name=ACHE;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=95010096; PubMed=7925428;
RA   Jbilo O., L'Hermite Y., Talesa V., Toutant J.-P., Chatonnet A.;
RT   "Acetylcholinesterase and butyrylcholinesterase expression in adult
RT   rabbit tissues and during development.";
RL   Eur. J. Biochem. 225:115-124(1994).
CC   -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: Homotetramer; composed of disulfide-linked homodimers.
CC       Interacts with PRIMA1. The interaction with PRIMA1 is required to
CC       anchor it to the basal lamina of cells and organize into tetramers
CC       (By similarity).
CC   -!- MISCELLANEOUS: Synapses usually contain asymmetric molecules of
CC       cholinesterase, with a collagen-like part disulfide-bonded to the
CC       catalytic part. A different, globular type of cholinesterase
CC       occurs on the outer surfaces of cell membranes, including those of
CC       erythrocytes.
CC   -!- MISCELLANEOUS: This is the catalytic subunit of an asymmetric or
CC       soluble form of ACHE.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; U05036; AAA53235.1; -.
DR   HSSP; P22303; 1F8U.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation;
KW   Serine esterase; Signal; Synapse.
FT   NON_TER       1      1
FT   SIGNAL       <1      1       Potential.
FT   CHAIN         2    584       Acetylcholinesterase.
FT   ACT_SITE    204    204       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    335    335       Charge relay system (By similarity).
FT   ACT_SITE    448    448       Charge relay system (By similarity).
FT   DISULFID     70     97       By similarity.
FT   DISULFID    258    273       By similarity.
FT   DISULFID    410    530       By similarity.
FT   DISULFID    581    581       Interchain (By similarity).
FT   CARBOHYD    266    266       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    351    351       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    465    465       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   584 AA;  64630 MW;  2AE157F3063649FE CRC64;

  Query Match             100.0%;  Score 87;  DB 1;  Length 584;
  Best Local Similarity   100.0%;  Pred. No. 0.0001;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        556 AEFHRWSSYMVHWK 569


RESULT 4
ACES_FELCA
ID   ACES_FELCA     STANDARD;      PRT;   611 AA.
AC   O62763; O62762;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN   Name=ACHE;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX   MEDLINE=20334351; PubMed=10874122; DOI=10.1016/S0006-2952(00)00365-8;
RA   Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA   Lockridge O.;
RT   "Determination of the DNA sequences of acetylcholinesterase and
RT   butyrylcholinesterase from cat and demonstration of the existence of
RT   both in cat plasma.";
RL   Biochem. Pharmacol. 60:479-487(2000).
CC   -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: Interacts with PRIMA1. The interaction with PRIMA1 is
CC       required to anchor it to the basal lamina of cells and organize
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CC       into tetramers (By similarity). Isoform H generates GPI-anchored
CC       dimers; disulfide linked. Isoform T generates multiple structures,
CC       ranging from monomers and dimers to collagen-tailed and
CC       hydrophobic-tailed forms, in which catalytic tetramers are
CC       associated with anchoring proteins that attach them to the basal
CC       lamina or to cell membranes. In the collagen-tailed forms, isoform
CC       T subunits are associated with a specific collagen, COLQ, which
CC       triggers the formation of isoform T tetramers, from monomers and
CC       dimers.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=T;
CC         IsoId=O62763-1; Sequence=Displayed;
CC       Name=H;
CC         IsoId=O62763-2; Sequence=VSP_001456;
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF053485; AAC08995.1; -.
DR   EMBL; AF053485; AAC08996.1; -.
DR   HSSP; P22303; 1F8U.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Alternative splicing; Glycoprotein; Hydrolase; Membrane;
KW   Neurotransmitter degradation; Serine esterase; Signal; Synapse.
FT   SIGNAL        1     31       By similarity.
FT   CHAIN        32    611       Acetylcholinesterase.
FT   ACT_SITE    231    231       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    362    362       Charge relay system (By similarity).
FT   ACT_SITE    475    475       Charge relay system (By similarity).
FT   DISULFID     97    124       By similarity.
FT   DISULFID    285    300       By similarity.
FT   DISULFID    437    557       By similarity.
FT   DISULFID    608    608       Interchain (By similarity).
FT   CARBOHYD    293    293       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    378    378       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    492    492       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    572    611       DTLDEAERQWKAEFHRWSSYMVHWKNQFDHYSKQDRCSDL
FT                                -> ASKAPSTCSGPAHGEAAPRPRPGLSLPLLLLLFLLLSR
FT                                LLR (in isoform H).
FT                                /FTId=VSP_001456.
SQ   SEQUENCE   611 AA;  67298 MW;  DFA5C0885A225527 CRC64;

  Query Match             100.0%;  Score 87;  DB 1;  Length 611;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        583 AEFHRWSSYMVHWK 596


RESULT 5
ACES_BOVIN
ID   ACES_BOVIN     STANDARD;      PRT;   613 AA.
AC   P23795; O97579;
DT   01-NOV-1991 (Rel. 20, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN   Name=ACHE;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC   TISSUE=Kidney;
RX   MEDLINE=98359754; PubMed=9693127;
RA   Mendelson I., Kronman C., Ariel N., Shafferman A., Velan B.;
RT   "Bovine acetylcholinesterase: cloning, expression and
RT   characterization.";
RL   Biochem. J. 334:251-259(1998).
RN   [2]
RP   SEQUENCE OF 31-613 (ISOFORM H).
RC   TISSUE=Fetal serum;
RX   MEDLINE=90306335; PubMed=2365060; DOI=10.1016/0014-5793(90)81522-P;
RA   Doctor B.P., Chapman T.C., Christner C.E., Deal C.D., de la Hoz D.M.,
RA   Gentry M.K., Ogert R.A., Rush R.S., Smyth K.K., Wolfe A.D.;
RT   "Complete amino acid sequence of fetal bovine serum
RT   acetylcholinesterase and its comparison in various regions with other
RT   cholinesterases.";
RL   FEBS Lett. 266:123-127(1990).
CC   -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: Interacts with PRIMA1. The interaction with PRIMA1 is
CC       required to anchor it to the basal lamina of cells and organize
CC       into tetramers (By similarity). Isoform H generates GPI-anchored
CC       dimers; disulfide linked. Isoform T generates multiple structures,
CC       ranging from monomers and dimers to collagen-tailed and
CC       hydrophobic-tailed forms, in which catalytic tetramers are
CC       associated with anchoring proteins that attach them to the basal
CC       lamina or to cell membranes. In the collagen-tailed forms, isoform
CC       T subunits are associated with a specific collagen, COLQ, which
CC       triggers the formation of isoform T tetramers, from monomers and
CC       dimers.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=T;
CC         IsoId=P23795-1; Sequence=Displayed;
CC       Name=H;
CC         IsoId=P23795-2; Sequence=VSP_001455;
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF061815; AAC64270.1; -.
DR   EMBL; AF061813; AAC64270.1; JOINED.
DR   EMBL; AF061814; AAC64270.1; JOINED.
DR   HSSP; P22303; 1F8U.
DR   GlycoSuiteDB; P23795; -.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Alternative splicing; Direct protein sequencing; Glycoprotein;
KW   Hydrolase; Membrane; Neurotransmitter degradation; Serine esterase;
KW   Signal; Synapse.
FT   SIGNAL        1     30
FT   CHAIN        31    613       Acetylcholinesterase.
FT   ACT_SITE    233    233       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    364    364       Charge relay system (By similarity).
FT   ACT_SITE    477    477       Charge relay system (By similarity).
FT   DISULFID     99    126       By similarity.
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FT   DISULFID    287    302       By similarity.
FT   DISULFID    439    559       By similarity.
FT   DISULFID    610    610       Interchain (By similarity).
FT   CARBOHYD     91     91       N-linked (GlcNAc. . .) (Probable).
FT   CARBOHYD    295    295       N-linked (GlcNAc. . .) (Probable).
FT   CARBOHYD    380    380       N-linked (GlcNAc. . .) (Probable).
FT   CARBOHYD    494    494       N-linked (GlcNAc. . .) (Probable).
FT   VARSPLIC    574    613       DTLDEAERQWKAEFHRWSSYMVHWKNQFDHYSKQDRCSDL
FT                                -> ASEAPCTCSGPAHGEAAPRPRPGLPLPLLLLLFLLSRL
FT                                LRL (in isoform H).
FT                                /FTId=VSP_001455.
FT   CONFLICT     46     46       R -> E (in Ref. 2).
FT   CONFLICT    169    169       T -> V (in Ref. 2).
FT   CONFLICT    212    212       W -> S (in Ref. 2).
FT   CONFLICT    323    323       S -> H (in Ref. 2).
FT   CONFLICT    352    352       H -> V (in Ref. 2).
FT   CONFLICT    424    424       L -> W (in Ref. 2).
FT   CONFLICT    524    524       D -> A (in Ref. 2).
FT   CONFLICT    549    554       EVRRGL -> GVPQAS (in Ref. 2).
FT   CONFLICT    571    571       S -> N (in Ref. 2).
SQ   SEQUENCE   613 AA;  67663 MW;  698D4F0DF8624B12 CRC64;

  Query Match             100.0%;  Score 87;  DB 1;  Length 613;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        585 AEFHRWSSYMVHWK 598


RESULT 6
ACES_HUMAN
ID   ACES_HUMAN     STANDARD;      PRT;   614 AA.
AC   P22303; Q16169; Q9BXP7;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN   Name=ACHE;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91088577; PubMed=2263619;
RA   Soreq H., Ben-Aziz R., Prody C.A., Seidman S., Gnatt A., Neville L.,
RA   Lieman-Hurwitz J., Lev-Lehman E., Ginzberg D., Lipidot-Lifson Y.,
RA   Zakut H.;
RT   "Molecular cloning and construction of the coding region for human
RT   acetylcholinesterase reveals a G + C-rich attenuating structure.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:9688-9692(1990).
RN   [2]
RP   SEQUENCE OF 521-614 FROM N.A.
RX   MEDLINE=21138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;
RA   Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA   Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA   Miller W., Koop B.F.;
RT   "Comparative analysis of the gene-dense ACHE/TFR2 region on human
RT   chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RL   Nucleic Acids Res. 29:1352-1365(2001).
RN   [3]
RP   PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
RX   MEDLINE=94131004; PubMed=8299725; DOI=10.1006/excr.1994.1039;
RA   Karpel R., Ben Aziz-Aloya R., Sternfeld M., Ehrlich G., Ginzberg D.,
RA   Tarroni P., Clementi F., Zakut H., Soreq H.;
RT   "Expression of three alternative acetylcholinesterase messenger RNAs
RT   in human tumor cell lines of different tissue origins.";
RL   Exp. Cell Res. 210:268-277(1994).
RN   [4]
RP   PARTIAL SEQUENCE.
RC   TISSUE=Erythrocyte;
RX   MEDLINE=89232136; PubMed=2714437; DOI=10.1016/0014-5793(89)81352-3;
RA   Chhajlani V., Derr D., Earles B., Schmell E., August T.;
RT   "Purification and partial amino acid sequence analysis of human
RT   erythrocyte acetylcholinesterase.";
RL   FEBS Lett. 247:279-282(1989).
RN   [5]
RP   MUTAGENESIS OF CYS-611.
RX   MEDLINE=92084699; PubMed=1748670;
RA   Velan B., Grosfeld H., Kronman C., Leitner M., Gozes Y., Lazar A.,
RA   Flashner Y., Marcus D., Cohen S., Shafferman A.;
RT   "The effect of elimination of intersubunit disulfide bonds on the
RT   activity, assembly, and secretion of recombinant human
RT   acetylcholinesterase. Expression of acetylcholinesterase Cys-580-->Ala
RT   mutant.";
RL   J. Biol. Chem. 266:23977-23984(1991).
RN   [6]
RP   MUTAGENESIS OF ACTIVE SITE RESIDUES AND OF ASP-206 AND ASP-435.
RX   MEDLINE=92388112; PubMed=1517212;
RA   Shafferman A., Kronman C., Flashner Y., Leitner M., Grosfeld H.,
RA   Ordentlich A., Gozes Y., Cohen S., Ariel N., Barak D.;
RT   "Mutagenesis of human acetylcholinesterase. Identification of residues
RT   involved in catalytic activity and in polypeptide folding.";
RL   J. Biol. Chem. 267:17640-17648(1992).
RN   [7]
RP   3D-STRUCTURE MODELING OF 35-574.
RX   MEDLINE=98304745; PubMed=9640563;
RA   Felder C.E., Botti S.A., Lifson S., Silman I., Sussman J.L.;
RT   "External and internal electrostatic potentials of cholinesterase
RT   models.";
RL   J. Mol. Graph. Model. 15:318-327(1997).
RN   [8]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 36-574.
RX   MEDLINE=20508217; PubMed=11053835; DOI=10.1107/S0907444900010659;
RA   Kryger G., Harel M., Giles K., Toker L., Velan B., Lazar A.,
RA   Kronman C., Barak D., Ariel N., Shafferman A., Silman I.,
RA   Sussman J.L.;
RT   "Structures of recombinant native and E202Q mutant human
RT   acetylcholinesterase complexed with the snake-venom toxin fasciculin-
RT   II.";
RL   Acta Crystallogr. D 56:1385-1394(2000).
RN   [9]
RP   VARIANT BLOOD GROUP YT(B) ASN-353.
RX   MEDLINE=93256075; PubMed=8488842;
RA   Bartels C.F., Zelinski T., Lockridge O.;
RT   "Mutation at codon 322 in the human acetylcholinesterase (ACHE) gene
RT   accounts for YT blood group polymorphism.";
RL   Am. J. Hum. Genet. 52:928-936(1993).
CC   -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: Homotetramer; composed of disulfide-linked homodimers.
CC       Interacts with PRIMA1. The interaction with PRIMA1 is required to
CC       anchor it to the basal lamina of cells and organize into tetramers
CC       (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=P22303-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P22303-2; Sequence=VSP_001457;
CC   -!- POLYMORPHISM: ACHE is responsible for the Yt blood group system.
CC       The molecular basis of the Yt(a)=Yt1/Yt(b)=Yt2 blood group
CC       antigens is a single variation in position 353; His-353
CC       corresponds to Yt(a) and the rare variant with Asn-353 to Yt(b).
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   -!- DATABASE: NAME=Blood group antigen mutation database;
CC       NOTE=Yt blood group system;
CC       WWW="http://www.bioc.aecom.yu.edu/bgmut/yt.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M55040; AAA68151.1; -.
DR   EMBL; AF312032; AAK21003.1; -.
DR   EMBL; S71129; AAC60618.1; -.
DR   PIR; A39256; A39256.
DR   PDB; 1B41; X-ray; A=36-574.
DR   PDB; 1F8U; X-ray; A=32-614.
DR   PDB; 2CLJ; Model; @=32-574.
DR   SWISS-2DPAGE; P22303; HUMAN.
DR   Genew; HGNC:108; ACHE.
DR   MIM; 100740; -.
DR   MIM; 112100; -.
DR   GO; GO:0005605; C:basal lamina; NAS.
DR   GO; GO:0005576; C:extracellular; TAS.
DR   GO; GO:0042166; F:acetylcholine binding; NAS.
DR   GO; GO:0003990; F:acetylcholinesterase activity; IMP.
DR   GO; GO:0001540; F:beta-amyloid binding; TAS.
DR   GO; GO:0042803; F:protein homodimerization activity; NAS.
DR   GO; GO:0001507; P:acetylcholine breakdown in synaptic cleft; NAS.
DR   GO; GO:0042982; P:amyloid precursor protein metabolism; TAS.
DR   GO; GO:0007155; P:cell adhesion; TAS.
DR   GO; GO:0008283; P:cell proliferation; TAS.
DR   GO; GO:0006260; P:DNA replication; TAS.
DR   GO; GO:0007517; P:muscle development; TAS.
DR   GO; GO:0050714; P:positive regulation of protein secretion; TAS.
DR   GO; GO:0009611; P:response to wounding; TAS.
DR   GO; GO:0007416; P:synaptogenesis; TAS.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   3D-structure; Alternative splicing; Blood group antigen;
KW   Direct protein sequencing; Glycoprotein; Hydrolase; Membrane;
KW   Neurotransmitter degradation; Polymorphism; Serine esterase; Signal;
KW   Synapse.
FT   SIGNAL       1     31       Potential.
FT   CHAIN       32    614       Acetylcholinesterase.
FT   ACT_SITE    234    234       Acyl-ester intermediate.
FT   ACT_SITE    365    365       Charge relay system.
FT   ACT_SITE    478    478       Charge relay system.
FT   DISULFID    100    127
FT   DISULFID    288    303
FT   DISULFID    440    560
FT   DISULFID    611    611       Interchain.
FT   CARBOHYD    296    296       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    381    381       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    495    495       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    575    614       DTLDEAERQWKAEFHRWSSYMVHWKNQFDHYSKQDRCSDL
FT                                -> GMQGPAGSAGRRGVGARQCNPSLLPLASEAPSTCPGFT
FT                                HGEAAPRPGLPLPLLLLHQLLLLFLSHLRRL (in
FT                                isoform 2).
FT                                /FTId=VSP_001457.
FT   VARIANT     333    333       V -> E (in dbSNP:8286).
FT                                /FTId=VAR_011934.
FT   VARIANT     353    353       H -> N (in Yt(b) antigen; dbSNP:1799805).
FT                                /FTId=VAR_002359.
FT   MUTAGEN     206    206       D->N: Misfolding, absence of secretion.
FT   MUTAGEN     234    234       S->A: Loss of activity.
FT   MUTAGEN     365    365       E->A: Loss of activity.
FT   MUTAGEN     435    435       D->N: Misfolding, absence of secretion.
FT   MUTAGEN     478    478       H->A: Loss of activity.
FT   MUTAGEN     611    611       C->A: Impairment of interchain disulfide
FT                                bridge formation.
FT   TURN         38     39
FT   STRAND       40     42
FT   STRAND       47     49
FT   STRAND       51     53
FT   TURN         56     57
FT   STRAND       60     67
FT   STRAND       69     70
FT   HELIX        74     76
FT   TURN         77     78
FT   STRAND       82     83
FT   STRAND       90     92
FT   STRAND       94     94
FT   STRAND       99    100
FT   TURN        109    110
FT   HELIX       112    115
FT   TURN        116    117
FT   STRAND      123    124
FT   STRAND      129    135

  Query Match            100.0%;  Score 87;  DB 1;  Length 614;
  Best Local Similarity  100.0%;  Pred. No. 0.00011;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 7
ACES_MOUSE
ID   ACES_MOUSE     STANDARD;      PRT;   614 AA.
AC   P21836;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN   Name=Ache;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90380429; PubMed=2400605; DOI=10.1016/0896-6273(90)90168-F;
RA   Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.;
RT   "Molecular cloning of mouse acetylcholinesterase: tissue distribution
RT   of alternatively spliced mRNA species.";
RL   Neuron 5:317-327(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RX   MEDLINE=21138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352;
RA   Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P.,
RA   Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C.,
RA   Miller W., Koop B.F.;
RT   "Comparative analysis of the gene-dense ACHE/TFR2 region on human
RT   chromosome 7q22 with the orthologous region on mouse chromosome 5.";
RL   Nucleic Acids Res. 29:1352-1365(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   INTERACTION WITH PRIMA1.
RX   MEDLINE=21664287; PubMed=11804574; DOI=10.1016/S0896-6273(01)00584-0;
RA   Perrier A.L., Massoulie J., Krejci E.;
RT   "PRiMA: the membrane anchor of acetylcholinesterase in the brain.";
RL   Neuron 33:275-285(2002).
RN   [5]
RP   X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) OF COMPLEX WITH FASCICULIN.
RX   MEDLINE=96067648; PubMed=8521480; DOI=10.1016/0092-8674(95)90128-0;
RA   Bourne Y., Taylor P., Marchot P.;
RT   "Acetylcholinesterase inhibition by fasciculin: crystal structure of
RT   the complex.";
RL   Cell 83:503-512(1995).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=99115643; PubMed=9915834; DOI=10.1074/jbc.274.5.2963;
RA   Bourne Y., Taylor P., Bougis P.E., Marchot P.;
RT   "Crystal structure of mouse acetylcholinesterase. A peripheral site-
RT   occluding loop in a tetrameric assembly.";
RL   J. Biol. Chem. 274:2963-2970(1999).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 34-573 IN COMPLEX WITH
RP   INHIBITOR.
RX   PubMed=12505979; DOI=10.1093/emboj/cdg005;
RA   Bourne Y., Taylor P., Radic Z., Marchot P.;
RT   "Structural insights into ligand interactions at the
RT   acetylcholinesterase peripheral anionic site.";
RL   EMBO J. 22:1-12(2003).
CC   -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: Isoform H generates GPI-anchored dimers; disulfide
CC       linked. Isoform T generates multiple structures, ranging from
CC       monomers and dimers to collagen-tailed and hydrophobic-tailed
CC       forms, in which catalytic tetramers are associated with anchoring
CC       proteins that attach them to the basal lamina or to cell
CC       membranes. In the collagen-tailed forms, isoform T subunits are
CC       associated with a specific collagen, COLQ, which triggers the
CC       formation of isoform T tetramers, from monomers and dimers (By
CC       similarity). Interacts with PRIMA1. The interaction with PRIMA1 is
CC       required to anchor it to the basal lamina of cells and organize
CC       into tetramers.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=T;
CC         IsoId=P21836-1; Sequence=Displayed;
CC       Name=H;
CC         IsoId=P21836-2; Sequence=Not described;
CC         Note=No experimental confirmation available;
CC   -!- TISSUE SPECIFICITY: Predominates in most expressing tissues except
CC       erythrocytes where a glycophospholipid-attached form of ACHE
CC       predominates.
CC   -!- MISCELLANEOUS: Synapses usually contain asymmetric molecules of
CC       cholinesterase, with a collagen-like part disulfide-bonded to the
CC       catalytic part. A different, globular type of cholinesterase
CC       occurs on the outer surfaces of cell membranes, including those of
CC       erythrocytes.
CC   -!- MISCELLANEOUS: This is the catalytic subunit of an asymmetric or
CC       soluble form of ACHE.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X56518; CAA39867.1; -.
DR   EMBL; AF312033; AAK28816.1; -.
DR   EMBL; BC046327; AAH46327.1; -.
DR   PIR; JH0314; JH0314.
DR   PDB; 1C2B; X-ray; A=35-573.
DR   PDB; 1C2O; X-ray; A/B/C/D=36-574.
DR   PDB; 1J06; X-ray; A/B=32-574.
DR   PDB; 1J07; X-ray; A/B=32-574.
DR   PDB; 1KU6; X-ray; A=32-580.
DR   PDB; 1MAA; X-ray; A/B/C/D=32-578.
DR   PDB; 1MAH; X-ray; A=32-574.
DR   PDB; 1N5M; X-ray; A/B=32-572.
DR   PDB; 1N5R; X-ray; A/B=32-574.
DR   PDB; 1Q83; X-ray; A/B=1-580.
DR   MGD; MGI:87876; Ache.
DR   GO; GO:0045202; C:synapse; IDA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   3D-structure; Alternative splicing; Glycoprotein; Hydrolase; Membrane;
KW   Neurotransmitter degradation; Serine esterase; Signal; Synapse.
FT   SIGNAL        1     31
FT   CHAIN        32    614       Acetylcholinesterase.
FT   ACT_SITE    234    234       Acyl-ester intermediate.
FT   ACT_SITE    365    365       Charge relay system.
FT   ACT_SITE    478    478       Charge relay system.
FT   DISULFID    100    127
FT   DISULFID    288    303
FT   DISULFID    440    560
FT   DISULFID    611    611       Interchain (By similarity).
FT   CARBOHYD    296    296       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    381    381       N-linked (GlcNAc. . .).
FT   CARBOHYD    495    495       N-linked (GlcNAc. . .).
FT   HELIX        37     39
FT   STRAND       40     43
FT   TURN         44     45
FT   STRAND       46     49
FT   STRAND       51     55
FT   TURN         56     57
FT   STRAND       58     67
FT   STRAND       69     69
FT   HELIX        74     76
FT   TURN         77     78
FT   STRAND       83     83
FT   STRAND       90     92
FT   STRAND       94     94
FT   STRAND       99    100
FT   TURN        109    110
FT   HELIX       112    115
FT   TURN        116    117
FT   STRAND      123    124
FT   STRAND      129    135
FT   STRAND      143    149
FT   TURN        153    155
FT   TURN        159    160
FT   HELIX       162    164
FT   HELIX       167    173
FT   STRAND      176    180
FT   HELIX       185    189
FT   TURN        193    194
FT   HELIX       202    217
FT   HELIX       218    221
FT   TURN        222    222
FT   STRAND      223    233
FT   TURN        234    234
FT   HELIX       235    244
FT   TURN        245    245
FT   HELIX       247    250
FT   TURN        251    252
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FT   STRAND      255    259
FT   STRAND      270    271
FT   HELIX       272    285
FT   TURN        286    287
FT   HELIX       297    304
FT   TURN        305    306
FT   HELIX       309    315

  Query Match             100.0%;  Score 87;  DB 1;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 8
ACES_RAT
ID   ACES_RAT       STANDARD;      PRT;   614 AA.
AC   P37136;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN   Name=Ache;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM T).
RX   MEDLINE=93107932; PubMed=8417155;
RA   Legay C., Bon S., Vernier P., Coussen F., Massoulie J.;
RT   "Cloning and expression of a rat acetylcholinesterase subunit:
RT   generation of multiple molecular forms and complementarity with a
RT   Torpedo collagenic subunit.";
RL   J. Neurochem. 60:337-346(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS H AND R).
RX   MEDLINE=93114454; PubMed=8417973; DOI=10.1016/0014-5793(93)81155-S;
RA   Legay C., Bon S., Massoulie J.;
RT   "Expression of a cDNA encoding the glycolipid-anchored form of rat
RT   acetylcholinesterase.";
RL   FEBS Lett. 315:163-166(1993).
CC   -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: Homotetramer; composed of disulfide-linked homodimers.
CC       Catalytic forms H (GPI-anchor dimer) and T (asymmetric collagen-
CC       tailed), which differ in their C-terminus, account for all types
CC       of known ACHE forms. Interacts with PRIMA1. The interaction with
CC       PRIMA1 is required to anchor it to the basal lamina of cells and
CC       organize into tetramers (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=T;
CC         IsoId=P37136-1; Sequence=Displayed;
CC       Name=H;
CC         IsoId=P37136-2; Sequence=VSP_001458;
CC       Name=R;
CC         IsoId=P37136-3; Sequence=VSP_001459;
CC         Note=May be not functional;
CC   -!- TISSUE SPECIFICITY: Has been found in central nervous system and
CC       muscle. Found in embryonic liver and spleen but not in adult
CC       liver.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S50879; AAB24586.1; -.
DR   EMBL; X70140; CAA49717.1; -.
DR   EMBL; X70141; CAA49718.1; -.
DR   PIR; JH0811; JH0811.
DR   HSSP; P21836; 1MAA.
DR   RGD; 69313; Ache.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Alternative splicing; Glycoprotein; Hydrolase; Membrane;
KW   Neurotransmitter degradation; Serine esterase; Signal; Synapse.
FT   SIGNAL        1     31       Potential.
FT   CHAIN        32    614       Acetylcholinesterase.
FT   ACT_SITE    234    234       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    365    365       Charge relay system (By similarity).
FT   ACT_SITE    478    478       Charge relay system (By similarity).
FT   DISULFID    100    127       By similarity.
FT   DISULFID    288    303       By similarity.
FT   DISULFID    440    560       By similarity.
FT   DISULFID    611    611       Interchain (By similarity).
FT   CARBOHYD    296    296       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    381    381       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    495    495       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    575    614       DTLDEAERQWKAEFHRWSSYMVHWKNQFDHYSKQERCSDL
FT                                -> ATEVPCTCPSPAHGEAAPRPGPALSLSLLFFLFLLHSG
FT                                LRWL (in isoform H).
FT                                /FTId=VSP_001458.
FT   VARSPLIC    575    614       DTLDEAERQWKAEFHRWSSYMVHWKNQFDHYSKQERCSDL
FT                                -> GRRGVGKQGMHKAARVGRTGERKGGKHRM (in
FT                                isoform R).
FT                                /FTId=VSP_001459.
SQ   SEQUENCE   614 AA;  68196 MW;  2EDAE7D46282E7C0 CRC64;

  Query Match             100.0%;  Score 87;  DB 1;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 9
Q67BC1
ID   Q67BC1       PRELIMINARY;      PRT;   614 AA.
AC   Q67BC1;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Acetylcholinesterase T-form.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cohen O., Kronman C., Velan B., Shafferman A.;
RT   "Macaca mulatta acetylcholinesterase gene.";
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR   EMBL; AY372522; AAR24295.1; JOINED.
DR   EMBL; AY372523; AAR24295.1; JOINED.
DR   EMBL; AY372526; AAR24295.1; -.
DR   EMBL; AY372524; AAR24295.1; JOINED.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
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DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
SQ   SEQUENCE   614 AA;  67772 MW;  7A4FCEE096015C5C CRC64;

  Query Match             100.0%;  Score 87;  DB 2;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00011;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 10
ACES_ELEEL
ID   ACES_ELEEL     STANDARD;      PRT;   633 AA.
AC   O42275;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
OS   Electrophorus electricus (Electric eel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC   Electrophoridae; Electrophorus.
OX   NCBI_TaxID=8005;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98070504; PubMed=9407087; DOI=10.1074/jbc.272.52.33045;
RA   Simon S., Massoulie J.;
RT   "Cloning and expression of acetylcholinesterase from Electrophorus.
RT   Splicing pattern of the 3' exons in vivo and in transfected mammalian
RT   cells.";
RL   J. Biol. Chem. 272:33045-33055(1997).
CC   -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF030422; AAB86606.1; -.
DR   HSSP; P04058; 1H23.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation;
KW   Serine esterase; Signal; Synapse.
FT   SIGNAL       1     23       Potential.
FT   CHAIN       24    633       Acetylcholinesterase.
FT   ACT_SITE    225    225       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    352    352       Charge relay system (By similarity).
FT   ACT_SITE    494    494       Charge relay system (By similarity).
FT   DISULFID     91    118       By similarity.
FT   DISULFID    279    290       By similarity.
FT   DISULFID    427    579       By similarity.
FT   DISULFID    630    630       Interchain (By similarity).
FT   CARBOHYD    133    133       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    184    184       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    283    283       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    368    368       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    511    511       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    591    591       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   633 AA;  71814 MW;  FC92FE7E4ADB84C3 CRC64;

  Query Match             96.6%;  Score 84;  DB 1;  Length 633;
  Best Local Similarity   92.9%;  Pred. No. 0.00031;
  Matches   13;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||:|||
Db        605 AEFHRWSSYMMHWK 618


RESULT 11
Q9W6Y8
ID   Q9W6Y8      PRELIMINARY;      PRT;    95 AA.
AC   Q9W6Y8;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Acetylcholinesterase (Fragment).
OS   Torpedo californica (Pacific electric ray).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
OC   Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OX   NCBI_TaxID=7787;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maulet Y., Camp S., Gibney G., Rachinsky T.L., Ekstroem T.J.,
RA   Taylor P.;
RL   Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR   EMBL; X56517; CAB37951.1; -.
DR   EMBL; X56516; CAB37951.1; JOINED.
DR   HSSP; P04058; 1EA5.
DR   InterPro; IPR002018; CarbesteraseB.
DR   Pfam; PF00135; COesterase; 1.
FT   NON_TER      1      1
SQ   SEQUENCE   95 AA;  11752 MW;  CA8F887A393E8508 CRC64;

  Query Match             92.0%;  Score 80;  DB 2;  Length 95;
  Best Local Similarity   92.3%;  Pred. No. 0.0002;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              |||||||||:|||
Db         68 EFHRWSSYMMHWK 80


RESULT 12
ACES_BRARE
ID   ACES_BRARE     STANDARD;      PRT;   634 AA.
AC   Q9DDE3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN   Name=ache;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20576389; PubMed=11016933; DOI=10.1074/jbc.M006308200;
RA   Bertrand C., Chatonnet A., Takke C., Yan Y., Postlethwait J.,
RA   Toutant J.-P., Cousin X.;
RT   "Zebrafish acetylcholinesterase is encoded by a single gene localized
RT   on linkage group 7. gene structure and polymorphism; molecular forms
RT   and expression pattern during development.";
RL   J. Biol. Chem. 276:464-474(2001).
CC   -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
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CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: Dimers and collagen-tailed forms, in which catalytic
CC       tetramers are associated with anchoring proteins that attach them
CC       to the basal lamina or to cell membranes. In the collagen-tailed
CC       forms, subunits are associated with a specific collagen, COLQ,
CC       which triggers the formation of isoform T tetramers from dimers.
CC   -!- MISCELLANEOUS: No other isoforms exist. This protein corresponds
CC       to the T isoform in other species.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ251640; CAC19790.1; -.
DR   HSSP; P04058; 1H23.
DR   ZFIN; ZDB-GENE-010906-1; ache.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation;
KW   Serine esterase; Signal; Synapse.
FT   SIGNAL        1     23       Potential.
FT   CHAIN        24    634       Acetylcholinesterase.
FT   ACT_SITE    225    225       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    352    352       Charge relay system (By similarity).
FT   ACT_SITE    495    495       Charge relay system (By similarity).
FT   DISULFID     91    118       By similarity.
FT   DISULFID    279    290       By similarity.
FT   DISULFID    427    580       By similarity.
FT   DISULFID    631    631       Interchain (By similarity).
FT   CARBOHYD    133    133       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    184    184       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    283    283       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    368    368       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    512    512       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    592    592       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   634 AA;  71998 MW;  47F348EA8A7C1E52 CRC64;

  Query Match             92.0%;  Score 80;  DB 1;  Length 634;
  Best Local Similarity   92.3%;  Pred. No. 0.0012;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              |||||||||:|||
Db        607 EFHRWSSYMMHWK 619


RESULT 13
ACES_BUNFA
ID   ACES_BUNFA     STANDARD;      PRT;   606 AA.
AC   Q92035; O73748; Q10720;
DT   01-NOV-1997 (Rel. 35, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
OS   Bungarus fasciatus (Banded krait).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Elapidae; Bungarinae; Bungarus.
OX   NCBI_TaxID=8613;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM S).
RC   TISSUE=Venom gland;
RX   MEDLINE=96279007; PubMed=8662867; DOI=10.1074/jbc.271.25.15099;
RA   Cousin X., Bon S., Duval N., Massoulie J., Bon C.;
RT   "Cloning and expression of acetylcholinesterase from Bungarus
RT   fasciatus venom. A new type of COOH-terminal domain; involvement of a
RT   positively charged residue in the peripheral site.";
RL   J. Biol. Chem. 271:15099-15108(1996).
RN   [2]
RP   SEQUENCE OF 512-606 FROM N.A. (ISOFORMS S AND T), SUBUNIT, AND TISSUE
RP   SPECIFICITY.
RC   TISSUE=Liver, and Muscle;
RX   MEDLINE=98212017; PubMed=9545320; DOI=10.1074/jbc.273.16.9812;
RA   Cousin X., Bon S., Massoulie J., Bon C.;
RT   "Identification of a novel type of alternatively spliced exon from the
RT   acetylcholinesterase gene of Bungarus fasciatus. Molecular forms of
RT   acetylcholinesterase in the snake liver and muscle.";
RL   J. Biol. Chem. 273:9812-9820(1998).
RN   [3]
RP   SEQUENCE OF 206-220; 253-272; 321-340; 347-372 AND 503-511.
RC   TISSUE=Venom;
RX   MEDLINE=96244524; PubMed=8674549; DOI=10.1016/0014-5793(96)00447-4;
RA   Cousin X., Creminon C., Grassi J., Meflah K., Cornu G., Saliou B.,
RA   Bon S., Massoulie J., Bon C.;
RT   "Acetylcholinesterase from Bungarus venom: a monomeric species.";
RL   FEBS Lett. 387:196-200(1996).
CC   -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: Isoform S is monomeric. Isoform T can form oligomers,
CC       including collagen-tailed forms.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=T;
CC         IsoId=Q92035-2; Sequence=Displayed;
CC       Name=S;
CC         IsoId=Q92035-1; Sequence=VSP_008215;
CC   -!- TISSUE SPECIFICITY: Liver and muscle contain both isoform T and
CC       isoform S. Venom gland predominantly contains isoform S.
CC   -!- PTM: The N-terminus is blocked.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   -!- CAUTION: It is uncertain whether Met-1 or Met-9 is the initiator.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U54591; AAC59905.1; -.
DR   EMBL; AF045238; AAC16420.1; -.
DR   EMBL; AF045238; AAC16421.1; -.
DR   HSSP; P04058; 1H23.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000908; Fish_Ache.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Alternative splicing; Direct protein sequencing; Glycoprotein;
KW   Hydrolase; Membrane; Neurotransmitter degradation; Serine esterase;
KW   Signal; Synapse.
FT   SIGNAL        1     28       Potential.
FT   CHAIN        29    606       Acetylcholinesterase.
FT   ACT_SITE    231    231       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    358    358       Charge relay system (By similarity).
FT   ACT_SITE    471    471       Charge relay system (By similarity).
FT   DISULFID     98    125       By similarity.
FT   DISULFID    285    296       By similarity.
FT   DISULFID    433    552       By similarity.
FT   DISULFID    603    603       Interchain (in isoform T) (By
FT                                similarity).
```

```
FT   CARBOHYD     289     289       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     374     374       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     484     484       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     564     564       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC     567     606       DNIEEAERQWKLEFHLWSAYMMHWKSQFDHYNKQDRCSEL
FT                                  -> VDPPRADRRRRSARA (in isoform S).
FT                                  /FTId=VSP_008215.
FT   MUTAGEN      101     101       M->Y: Increases peripheral site ligand
FT                                  binding.
FT   MUTAGEN      316     316       K->D: Increases peripheral site ligand
FT                                  binding.
FT   CONFLICT     268     268       T -> S (in Ref. 3).
FT   CONFLICT     350     350       V -> L (in Ref. 3).
SQ   SEQUENCE   606 AA;  68074 MW;  B95998AEEA0E5709 CRC64;

  Query Match             80.5%;  Score 70;  DB 1;  Length 606;
  Best Local Similarity   76.9%;  Pred. No. 0.035;
  Matches   10;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              ||| ||:||:|||
Db        579 EFHLWSAYMMHWK 591


RESULT 14
Q9JKC1
ID   Q9JKC1      PRELIMINARY;      PRT;   597 AA.
AC   Q9JKC1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Butyrylcholinesterase.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Li B., Stribley J., Ticu A., Xie W., Schopfer L.M., Hammond P.,
RA   Brimijoin S., Hinrichs S.H., Lockridge O.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Ticu A.M., Lockridge O., Bartels C.F.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR   EMBL; AF244349; AAF44713.1; -.
DR   HSSP; P06276; 1P0I.
DR   GO; GO:0004104; F:cholinesterase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase.
SQ   SEQUENCE   597 AA;  67776 MW;  771204D166C7EEAC CRC64;

  Query Match             74.7%;  Score 65;  DB 2;  Length 597;
  Best Local Similarity   71.4%;  Pred. No. 0.19;
  Matches   10;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | |||||:||: ||
Db        568 AGFHRWSNYMMDWK 581


RESULT 15
ACES_CHICK
ID   ACES_CHICK     STANDARD;      PRT;   767 AA.
AC   P36196;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
GN   Name=ACHE;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=94325359; PubMed=8049273; DOI=10.1016/0167-4781(94)90204-6;
RA   Randall W.R., Rimer M., Gough N.R.;
RT   "Cloning and analysis of chicken acetylcholinesterase transcripts from
RT   muscle and brain.";
RL   Biochim. Biophys. Acta 1218:453-456(1994).
CC   -!- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC   -!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC   -!- SUBUNIT: Oligomer composed of disulfide-linked homodimers.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U03472; AAA60456.1; -.
DR   PIR; S47639; S47639.
DR   HSSP; P21836; 1N5M.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Glycoprotein; Hydrolase; Membrane; Neurotransmitter degradation;
KW   Serine esterase; Signal; Synapse.
FT   SIGNAL        1     19       Potential.
FT   CHAIN        20    767       Acetylcholinesterase.
FT   ACT_SITE    227    227       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    520    520       Charge relay system (By similarity).
FT   ACT_SITE    633    633       Charge relay system (By similarity).
FT   DISULFID     94    121       By similarity.
FT   DISULFID    281    292       By similarity.
FT   DISULFID    595    713       By similarity.
FT   DISULFID    764    764       Interchain (By similarity).
FT   CARBOHYD    285    285       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    536    536       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    650    650       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    725    725       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   767 AA;  83020 MW;  B1B3DF29C31F6062 CRC64;

  Query Match             74.7%;  Score 65;  DB 1;  Length 767;
  Best Local Similarity   76.9%;  Pred. No. 0.24;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              |||||||||  |:
Db        740 EFHRWSSYMGRWR 752


RESULT 16
Q96HL2
ID   Q96HL2      PRELIMINARY;      PRT;    64 AA.
AC   Q96HL2;
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DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   BCHE protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC008396; AAH08396.1; -.
DR   HSSP; P06276; 1P0I.
SQ   SEQUENCE   64 AA;  7861 MW;  67A0BB38F441F05F CRC64;

  Query Match             71.3%;  Score 62;  DB 2;  Length 64;
  Best Local Similarity   64.3%;  Pred. No. 0.064;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db         35 AGFHRWNNYMMDWK 48


RESULT 17
CHLE_HORSE
ID   CHLE_HORSE     STANDARD;      PRT;   574 AA.
AC   P81908;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Cholinesterase (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline
DE   esterase II) (Butyrylcholine esterase) (Pseudocholinesterase) (EQ-
DE   BCHE).
GN   Name=BCHE;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Plasma;
RA   Moorad D.R., Luo C., Garcia G.E., Doctor B.P.;
RT   "Amino acid sequence of horse serum butyrycholinesterase.";
RL   (In) Doctor B.P., Taylor P., Quinn D.M., Rotundo R.L., Gentry M.K.
RL   (eds.);
RL   Structure and function of cholinesterases and related proteins,
RL   pp.145-146, Plenum Press, New York and London (1998).
CC   -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC       carboxylic acid anion.
CC   -!- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC       two subunits in a dimer are linked by a disulfide bond.
CC   -!- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC   -!- MISCELLANEOUS: Cholinesterase is highly reactive with
CC       organophosphate esters.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR   HSSP; P21836; 1N5M.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Direct protein sequencing; Glycoprotein; Hydrolase; Serine esterase.
FT   ACT_SITE    198    198       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    325    325       Charge relay system (By similarity).
FT   ACT_SITE    438    438       Charge relay system (By similarity).
FT   DISULFID     65     92       By similarity.
FT   DISULFID    252    263       By similarity.
FT   DISULFID    400    519       By similarity.
FT   DISULFID    571    571       Interchain (By similarity).
FT   CARBOHYD     57     57       N-linked (GlcNAc. . .).
FT   CARBOHYD    106    106       N-linked (GlcNAc. . .).
FT   CARBOHYD    241    241       N-linked (GlcNAc. . .).
FT   CARBOHYD    256    256       N-linked (GlcNAc. . .).
FT   CARBOHYD    341    341       N-linked (GlcNAc. . .).
FT   CARBOHYD    455    455       N-linked (GlcNAc. . .).
FT   CARBOHYD    481    481       N-linked (GlcNAc. . .).
FT   CARBOHYD    486    486       N-linked (GlcNAc. . .).
SQ   SEQUENCE   574 AA;  65641 MW;  07755EE9FB9CB33E CRC64;

  Query Match             71.3%;  Score 62;  DB 1;  Length 574;
  Best Local Similarity   64.3%;  Pred. No. 0.51;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        545 AGFHRWNNYMMDWK 558


RESULT 18
CHLE_HUMAN
ID   CHLE_HUMAN     STANDARD;      PRT;   602 AA.
AC   P06276;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE   (Choline esterase II) (Butyrylcholine esterase)
DE   (Pseudocholinesterase).
GN   Name=BCHE; Synonyms=CHE1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90212557; PubMed=2322535;
RA   Arpagaus M., Kott M., Vatsis K.P., Bartels C.F., la Du B.N.,
RA   Lockridge O.;
RT   "Structure of the gene for human butyrylcholinesterase. Evidence for a
RT   single copy.";
RL   Biochemistry 29:124-131(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal;
RX   MEDLINE=87231856; PubMed=3035536;
RA   Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O., Soreq H.;
RT   "Isolation and characterization of full-length cDNA clones coding for
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RT   cholinesterase from fetal human tissues.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=88016155; PubMed=3477799;
RA   McTiernan C., Adkins S., Chatonnet A., Vaughan T.A., Bartels C.F.,
RA   Kott M., Rosenberry T.L., la Du B.N., Lockridge O.;
RT   "Brain cDNA clone for human cholinesterase.";
RL   Proc. Natl. Acad. Sci. U.S.A. 84:6682-6686(1987).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   SEQUENCE OF 29-602.
RC   TISSUE=Plasma;
RX   MEDLINE=87109144; PubMed=3542989;
RA   Lockridge O., Bartels C.F., Vaughan T.A., Wong C.K., Norton S.E.,
RA   Johnson L.L.;
RT   "Complete amino acid sequence of human serum cholinesterase.";
RL   J. Biol. Chem. 262:549-557(1987).
RN   [6]
RP   DISULFIDE BONDS.
RX   MEDLINE=88007487; PubMed=3115973;
RA   Lockridge O., Adkins S., la Du B.N.;
RT   "Location of disulfide bonds within the sequence of human serum
RT   cholinesterase.";
RL   J. Biol. Chem. 262:12945-12952(1987).
RN   [7]
RP   REVIEW.
RX   MEDLINE=89149758; PubMed=3067729;
RA   Lockridge O.;
RT   "Structure of human serum cholinesterase.";
RL   Bioessays 9:125-128(1988).
RN   [8]
RP   VARIANT ATYPICAL GLY-98.
RX   MEDLINE=89128896; PubMed=2915989;
RA   McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra A.,
RA   van der Spek A.F.L., Lockridge O., la Du B.N.;
RT   "Identification of the structural mutation responsible for the
RT   dibucaine-resistant (atypical) variant form of human serum
RT   cholinesterase.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:953-957(1989).
RN   [9]
RP   VARIANT ILE-358.
RX   MEDLINE=96287386; PubMed=8680411;
RA   Iida S., Kinoshita M., Fujii H., Moriyama Y., Nakamura Y., Yura N.,
RA   Moriwaki K.;
RT   "Mutations of human butyrylcholinesterase gene in a family with
RT   hypocholinesterasemia.";
RL   Hum. Mutat. 6:349-351(1995).
CC   -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC       carboxylic acid anion.
CC   -!- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC       two subunits in a dimer are linked by a disulfide bond.
CC   -!- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC   -!- DISEASE: Mutant alleles of CHE1 are responsible for
CC       hypocholinesterasemia resulting in suxamethonium sensitivity.
CC       Homozygous persons sustain prolonged apnea after administration of
CC       the muscle relaxant suxamethonium in connection with surgical
CC       anesthesia.
CC   -!- MISCELLANEOUS: Cholinesterase is highly reactive with
CC       organophosphate esters.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M32391; AAA99296.1; -.
DR   EMBL; M32389; AAA99296.1; JOINED.
DR   EMBL; M32390; AAA99296.1; JOINED.
DR   EMBL; M16541; AAA98113.1; -.
DR   EMBL; M16474; AAA52015.1; -.
DR   EMBL; BC018141; AAH18141.1; -.
DR   PIR; A33769; ACHU.
DR   PDB; 1EHO; Model; A=30-560.
DR   PDB; 1EHQ; Model; A=30-560.
DR   PDB; 1P0I; X-ray; A=29-557.
DR   PDB; 1P0M; X-ray; A=29-557.
DR   PDB; 1P0P; X-ray; A=29-557.
DR   PDB; 1P0Q; X-ray; A=29-557.
DR   Genew; HGNC:983; BCHE.
DR   H-InvDB; HIX0003828; -.
DR   MIM; 177400; -.
DR   GO; GO:0001540; F:beta-amyloid binding; NAS.
DR   GO; GO:0003824; F:catalytic activity; NAS.
DR   GO; GO:0004104; F:cholinesterase activity; NAS.
DR   GO; GO:0019899; F:enzyme binding; NAS.
DR   GO; GO:0050783; P:cocaine metabolism; TAS.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   3D-structure; Direct protein sequencing; Disease mutation;
KW   Glycoprotein; Hydrolase; Polymorphism; Serine esterase; Signal.
FT   SIGNAL       1     28
FT   CHAIN       29    602       Cholinesterase.
FT   ACT_SITE    226    226       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    353    353       Charge relay system (By similarity).
FT   ACT_SITE    466    466       Charge relay system (By similarity).
FT   DISULFID     93    120
FT   DISULFID    280    291
FT   DISULFID    428    547
FT   DISULFID    599    599       Interchain.
FT   CARBOHYD     45     45       N-linked (GlcNAc. . .).
FT   CARBOHYD     85     85       N-linked (GlcNAc. . .).
FT   CARBOHYD    134    134       N-linked (GlcNAc. . .).
FT   CARBOHYD    269    269       N-linked (GlcNAc. . .).
FT   CARBOHYD    284    284       N-linked (GlcNAc. . .).
FT   CARBOHYD    369    369       N-linked (GlcNAc. . .).
FT   CARBOHYD    483    483       N-linked (GlcNAc. . .).
FT   CARBOHYD    509    509       N-linked (GlcNAc. . .).
FT   CARBOHYD    514    514       N-linked (GlcNAc. . .).
FT   VARIANT      98     98       D -> G (in atypical form, dibucaine-
FT                                resistant; dbSNP:1799807).
FT                                /FTId=VAR_002360.
FT   VARIANT     271    271       T -> M (in fluoride-1).
```

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FT                              /FTId=VAR_002361.
FT   VARIANT     358    358     L -> I (in hypocholinesterasemia).
FT                              /FTId=VAR_002362.
FT   VARIANT     418    418     G -> V (in fluoride-2).
FT                              /FTId=VAR_002363.
FT   VARIANT     567    567     A -> T (in K variant; with reduced enzyme
FT                              activity; dbSNP:1803274).
FT                              /FTId=VAR_002364.
SQ   SEQUENCE   602 AA;  68418 MW;  C9836409D9057F27 CRC64;

  Query Match             71.3%;  Score 62;  DB 1;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.54;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 19
Q9N1N9
ID   Q9N1N9      PRELIMINARY;      PRT;   602 AA.
AC   Q9N1N9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Butyrylcholinesterase (EC 3.1.1.8).
GN   Name=BCHE;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20181263; PubMed=10718335; DOI=10.1016/S0006-2952(99)00389-5;
RA   Wierdl M., Morton C.L., Danks M.K., Potter P.M.;
RT   "Isolation and characterization of a cDNA encoding a horse liver
RT   butyrylcholinesterase: evidence for CPT-11 drug activation.";
RL   Biochem. Pharmacol. 59:773-781(2000).
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR   EMBL; AF178685; AAF61480.1; -.
DR   HSSP; P06276; 1P0P.
DR   GO; GO:0004104; F:cholinesterase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase.
SQ   SEQUENCE   602 AA;  68838 MW;  94C73F00431DF26E CRC64;

  Query Match             71.3%;  Score 62;  DB 2;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.54;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 20
Q90ZK8
ID   Q90ZK8      PRELIMINARY;      PRT;   603 AA.
AC   Q90ZK8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Butyrylcholinesterase precursor (EC 3.1.1.8).
GN   Name=BCHE;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Geissler K., Chatonnet A., Layer P.G.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
DR   EMBL; AJ306928; CAC37792.1; -.
DR   HSSP; P06276; 1P0I.
DR   GO; GO:0004104; F:cholinesterase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase; Signal.
FT   SIGNAL        1     29       Potential.
FT   CHAIN        30    603       butyrylcholinesterase.
SQ   SEQUENCE   603 AA;  68480 MW;  A350FDDF68574ADF CRC64;

  Query Match             71.3%;  Score 62;  DB 2;  Length 603;
  Best Local Similarity   64.3%;  Pred. No. 0.54;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 21
CHLE_RABIT
ID   CHLE_RABIT     STANDARD;      PRT;   581 AA.
AC   P21927;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE   (Choline esterase II) (Butyrylcholine esterase)
DE   (Pseudocholinesterase).
GN   Name=BCHE;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=New Zealand;
RX   MEDLINE=90326526; PubMed=2374720;
RA   Jbilo O., Roudani S., Chatonnet A.;
RT   "Complete sequence of rabbit butyrylcholinesterase.";
RL   Nucleic Acids Res. 18:3990-3990(1990).
RN   [2]
RP   SEQUENCE OF 75-215 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=91201348; PubMed=2016308;
RA   Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA   Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;
RT   "Use of the polymerase chain reaction for homology probing of
RT   butyrylcholinesterase from several vertebrates.";
RL   J. Biol. Chem. 266:6966-6974(1991).
CC   -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC       carboxylic acid anion.
CC   -!- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC       two subunits in a dimer are linked by a disulfide bond.
CC   -!- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC   -!- MISCELLANEOUS: Cholinesterase is highly reactive with
CC       organophosphate esters.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X52090; CAA36308.1; -.
DR   EMBL; X52091; CAA36308.1; JOINED.
DR   EMBL; X52092; CAA36308.1; JOINED.
DR   EMBL; M62779; AAA31169.1; -.
DR   PIR; S10255; C39768.
DR   HSSP; P22303; 1F8U.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Glycoprotein; Hydrolase; Serine esterase; Signal.
FT   SIGNAL        1      8       Potential.
FT   CHAIN         9    581       Cholinesterase.
FT   ACT_SITE    205    205       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    332    332       Charge relay system (By similarity).
FT   ACT_SITE    445    445       Charge relay system (By similarity).
FT   DISULFID     72     99       By similarity.
FT   DISULFID    259    270       By similarity.
FT   DISULFID    407    526       By similarity.
FT   DISULFID    578    578       Interchain (By similarity).
FT   CARBOHYD     64     64       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    113    113       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    248    248       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    263    263       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    348    348       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    462    462       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    488    488       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    492    492       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    493    493       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   581 AA;  66156 MW;  FE8B199E7B32EB0A CRC64;

  Query Match             70.1%;  Score 61;  DB 1;  Length 581;
  Best Local Similarity   64.3%;  Pred. No. 0.73;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        552 AGFHRWNNYMMAWK 565


RESULT 22
CHLE_MOUSE
ID   CHLE_MOUSE     STANDARD;      PRT;   603 AA.
AC   Q03311;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE   (Choline esterase II) (Butyrylcholine esterase)
DE   (Pseudocholinesterase).
GN   Name=Bche;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90380429; PubMed=2400605; DOI=10.1016/0896-6273(90)90168-F;
RA   Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Taylor P.;
RT   "Molecular cloning of mouse acetylcholinesterase: tissue distribution
RT   of alternatively spliced mRNA species.";
RL   Neuron 5:317-327(1990).
RN   [2]
RP   SEQUENCE OF 97-237 FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=91201348; PubMed=2016308;
RA   Arpagaus M., Chatonnet A., Masson P., Newton M., Vaughan T.A.,
RA   Bartels C.F., Nogueira C.P., la Du B.N., Lockridge O.;
RT   "Use of the polymerase chain reaction for homology probing of
RT   butyrylcholinesterase from several vertebrates.";
RL   J. Biol. Chem. 266:6966-6974(1991).
CC   -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC       carboxylic acid anion.
CC   -!- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC       two subunits in a dimer are linked by a disulfide bond.
CC   -!- TISSUE SPECIFICITY: Present in most cells except erythrocytes.
CC   -!- MISCELLANEOUS: Cholinesterase is highly reactive with
CC       organophosphate esters.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M99492; AAA37328.1; -.
DR   PIR; S70849; S70849.
DR   HSSP; P22303; 1F8U.
DR   MGD; MGI:894278; Bche.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Glycoprotein; Hydrolase; Serine esterase; Signal.
FT   SIGNAL        1     29
FT   CHAIN        30    603       Cholinesterase.
FT   ACT_SITE    227    227       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    354    354       Charge relay system (By similarity).
FT   ACT_SITE    467    467       Charge relay system (By similarity).
FT   DISULFID     94    121       By similarity.
FT   DISULFID    281    292       By similarity.
FT   DISULFID    429    548       By similarity.
FT   DISULFID    600    600       Interchain (By similarity).
FT   CARBOHYD     86     86       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    135    135       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    270    270       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    370    370       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    484    484       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    510    510       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    515    515       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT    129    129       R -> P (in Ref. 2).
SQ   SEQUENCE   603 AA;  68521 MW;  719B1B220D1E5367 CRC64;

  Query Match             70.1%;  Score 61;  DB 1;  Length 603;
  Best Local Similarity   64.3%;  Pred. No. 0.76;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | |||||:||: |:
Db        574 AGFHRWSNYMMDWQ 587


RESULT 23
CHLE_FELCA
ID   CHLE_FELCA     STANDARD;      PRT;   602 AA.
AC   O62760;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE   (Choline esterase II) (Butyrylcholine esterase)
```

```
DE   (Pseudocholinesterase).
GN   Name=BCHE;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary;
RX   MEDLINE=20334351; PubMed=10874122; DOI=10.1016/S0006-2952(00)00365-8;
RA   Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA   Lockridge O.;
RT   "Determination of the DNA sequences of acetylcholinesterase and
RT   butyrylcholinesterase from cat and demonstration of the existence of
RT   both in cat plasma.";
RL   Biochem. Pharmacol. 60:479-487(2000).
CC   -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC       carboxylic acid anion.
CC   -!- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC       two subunits in a dimer are linked by a disulfide bond (By
CC       similarity).
CC   -!- MISCELLANEOUS: Cholinesterase is highly reactive with
CC       organophosphate esters (By similarity).
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF053483; AAC06261.1; -.
DR   HSSP; P22303; 1B41.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Glycoprotein; Hydrolase; Serine esterase; Signal.
FT   SIGNAL        1     28       Potential.
FT   CHAIN        29    602       Cholinesterase.
FT   ACT_SITE    226    226       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    353    353       Charge relay system (By similarity).
FT   ACT_SITE    466    466       Charge relay system (By similarity).
FT   DISULFID     93    120       By similarity.
FT   DISULFID    280    291       By similarity.
FT   DISULFID    428    547       By similarity.
FT   DISULFID    599    599       Interchain (By similarity).
FT   CARBOHYD     85     85       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    134    134       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    269    269       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    284    284       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    369    369       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    483    483       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    509    509       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    513    513       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    514    514       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   602 AA;  68328 MW;  ECB8879232B74B9C CRC64;

  Query Match             64.4%;  Score 56;  DB 1;  Length 602;
  Best Local Similarity   57.1%;  Pred. No. 4.2;
  Matches    8;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | |:||::||: ||
Db        573 AGFYRWNNYMMDWK 586


RESULT 24
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CHLE_PANTT
ID   CHLE_PANTT     STANDARD;      PRT;   602 AA.
AC   O62761;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Cholinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
DE   (Choline esterase II) (Butyrylcholine esterase)
DE   (Pseudocholinesterase).
GN   Name=BCHE;
OS   Panthera tigris tigris (Bengal tiger).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Panthera.
OX   NCBI_TaxID=74535;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary;
RX   MEDLINE=20334351; PubMed=10874122; DOI=10.1016/S0006-2952(00)00365-8;
RA   Bartels C.F., Xie W., Miller-Lindholm A.K., Schopfer L.M.,
RA   Lockridge O.;
RT   "Determination of the DNA sequences of acetylcholinesterase and
RT   butyrylcholinesterase from cat and demonstration of the existence of
RT   both in cat plasma.";
RL   Biochem. Pharmacol. 60:479-487(2000).
CC   -!- CATALYTIC ACTIVITY: An acylcholine + H(2)O = choline + a
CC       carboxylic acid anion.
CC   -!- SUBUNIT: Homotetramer. The tetramer is composed of two dimers. The
CC       two subunits in a dimer are linked by a disulfide bond (By
CC       similarity).
CC   -!- MISCELLANEOUS: Cholinesterase is highly reactive with
CC       organophosphate esters (By similarity).
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF053484; AAC06262.1; -.
DR   HSSP; P22303; 1B41.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Glycoprotein; Hydrolase; Serine esterase; Signal.
FT   SIGNAL        1     28       Potential.
FT   CHAIN        29    602       Cholinesterase.
FT   ACT_SITE    226    226       Acyl-ester intermediate (By similarity).
FT   ACT_SITE    353    353       Charge relay system (By similarity).
FT   ACT_SITE    466    466       Charge relay system (By similarity).
FT   DISULFID     93    120       By similarity.
FT   DISULFID    280    291       By similarity.
FT   DISULFID    428    547       By similarity.
FT   DISULFID    599    599       Interchain (By similarity).
FT   CARBOHYD     85     85       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    134    134       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    269    269       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    284    284       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    369    369       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    483    483       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    509    509       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    513    513       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    514    514       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   602 AA;  68289 MW;  EB0C8B9148E956A1 CRC64;

  Query Match             64.4%;  Score 56;  DB 1;  Length 602;
  Best Local Similarity   57.1%;  Pred. No. 4.2;
```

```
  Matches    8;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | |:||::||: ||
Db        573 AGFYRWNNYMMDWK 586


RESULT 25
Q8B0J7
ID   Q8B0J7      PRELIMINARY;      PRT;   205 AA.
AC   Q8B0J7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Protein N (Fragment).
OS   California encephalitis serogroup virus LEIV.
OC   Viruses; ssRNA negative-strand viruses; Bunyaviridae; Orthobunyavirus.
OX   NCBI_TaxID=178787;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22295875; PubMed=12408673;
RA   Vanlandingham D.L., Davis B.S., Lvov D.K., Samokhvalov E., Lvov S.D.,
RA   Black W.C., Higgs S., Beaty B.J.;
RT   "Molecular characterization of California serogroup viruses isolated
RT   in Russia.";
RL   Am. J. Trop. Med. Hyg. 67:306-309(2002).
DR   EMBL; AF392980; AAN60739.1; -.
DR   GO; GO:0019013; C:viral nucleocapsid; IEA.
DR   InterPro; IPR001784; Bunya_nucleocap.
DR   Pfam; PF00952; Bunya_nucleocap; 1.
DR   ProDom; PD001909; Bunya_nucleocap; 1.
FT   NON_TER     205     205
SQ   SEQUENCE   205 AA;  23619 MW;  0A66C083F25A1491 CRC64;

  Query Match             55.2%;  Score 48;  DB 2;  Length 205;
  Best Local Similarity   60.0%;  Pred. No. 23;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 HRWSSYMVHW 13
              |||| |:  |
Db         93 HRWSGYLARW 102


RESULT 26
Q7RTL7
ID   Q7RTL7      PRELIMINARY;      PRT;   550 AA.
AC   Q7RTL7;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Actylcholinesterase (EC 3.1.1.7) (Fragment).
GN   Name=achE;
OS   Ciona savignyi.
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC   Phlebobranchia; Cionidae; Ciona.
OX   NCBI_TaxID=51511;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22284560; PubMed=12396499; DOI=10.1098/rspb.2002.2122;
RA   Weill M., Fort P., Berthomi eu A., Dubois M.P., Pasteur N.,
RA   Raymond M.;
RT   "A novel acetylcholinesterase gene in mosquitoes codes for the
RT   insecticide target and is non-homologous to the ace gene in
RT   Drosophila.";
RL   Proc. R. Soc. Lond., B, Biol. Sci. 269:2007-2016(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Fort P.P.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC   -!- MISCELLANEOUS: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ third party annotation (TPA) entry.
DR   EMBL; BN000070; CAD29868.1; -.
DR   HSSP; P21836; 1J07.
DR   GO; GO:0003990; F:acetylcholinesterase activity; IEA.
DR   GO; GO:0004104; F:cholinesterase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   InterPro; IPR002018; CarbesteraseB.
DR   InterPro; IPR000997; Cholinesterase.
DR   InterPro; IPR000379; Ser_estrs.
DR   Pfam; PF00135; COesterase; 1.
DR   PRINTS; PR00878; CHOLNESTRASE.
DR   PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR   PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW   Hydrolase.
FT   NON_TER       1       1
SQ   SEQUENCE   550 AA;  61942 MW;  4494459852A39C0A CRC64;

  Query Match             54.0%;  Score 47;  DB 2;  Length 550;
  Best Local Similarity   66.7%;  Pred. No. 83;
  Matches    8;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHW 13
              ||||||  |  |
Db        521 EFHRWSESMDLW 532


RESULT 27
Q64NA7
ID   Q64NA7      PRELIMINARY;      PRT;   667 AA.
AC   Q64NA7;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative helicase.
GN   ORFNames=BF4288;
OS   Bacteroides fragilis.
OC   Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC   Bacteroidaceae; Bacteroides.
OX   NCBI_TaxID=817;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=YCH46;
RA   Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA   Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT   "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT   inversions regulating cell surface adaptation.";
RL   Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DR   EMBL; AP006841; BAD51028.1; -.
KW   Helicase.
SQ   SEQUENCE   667 AA;  76735 MW;  6DB01B9A729516C9 CRC64;

  Query Match             53.4%;  Score 46.5;  DB 2;  Length 667;
  Best Local Similarity   69.2%;  Pred. No. 1.2e+02;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          3 FHRWSSYMV-HWK 14
              ||||   || |||
Db        405 FHRWFLSMVAHWK 417


RESULT 28
Q759Y3
ID   Q759Y3      PRELIMINARY;      PRT;   709 AA.
AC   Q759Y3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   ADR140Cp.
GN   ORFNames=ADR140C;
OS   Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX   NCBI_TaxID=33169;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   STRAIN=ATCC 10895;
RA   Voegeli S.E., Brachat S., Dietrich F.S., Lerch A., Gaffney T.,
RA   Philippsen P.;
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE016817; AAS52060.1; -.
DR   AGD; ADR140C; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   InterPro; IPR001410; DEAD.
DR   InterPro; IPR011545; DEAD/DEAH_N.
DR   InterPro; IPR001650; Helicase_C.
DR   Pfam; PF00270; DEAD; 1.
DR   Pfam; PF00271; Helicase_C; 1.
DR   SMART; SM00487; DEXDc; 1.
DR   SMART; SM00490; HELICc; 1.
KW   ATP-binding; Helicase; Hydrolase.
SQ   SEQUENCE   709 AA;  78654 MW;  0B78934D3DF69F09 CRC64;

  Query Match             51.7%;  Score 45;  DB 2;  Length 709;
  Best Local Similarity   35.7%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    7;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              |: ||::: ::||:
Db        584 AQLHRYAAALLHWR 597


RESULT 29
Q857V6
ID   Q857V6      PRELIMINARY;      PRT;   143 AA.
AC   Q857V6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Gp56.
OS   Mycobacteriophage CJW1.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX   NCBI_TaxID=205869;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
RA   Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
RA   Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
RA   Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
RA   Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA   Hatfull G.F.;
RT   "Origins of highly mosaic mycobacteriophage genomes.";
RL   Cell 113:171-182(2003).
DR   EMBL; AY129331; AAN01670.1; -.
DR   InterPro; IPR010982; Lambda_like_DNA.
SQ   SEQUENCE   143 AA;  15905 MW;  CBCAD8876CBBF876 CRC64;

  Query Match             50.6%;  Score 44;  DB 2;  Length 143;
  Best Local Similarity   46.2%;  Pred. No. 64;
  Matches    6;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHW 13
              |:  |||:|:: |
Db         11 ADRDRWSTYVIDW 23


RESULT 30
O78318
ID   O78318      PRELIMINARY;      PRT;   260 AA.
AC   O78318;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   NADH dehydrogenase subunit F (Fragment).
GN   Name=ndhF;
OS   Arabidopsis thaliana (Mouse-ear cress).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99003705; PubMed=9787437;
RA   Galloway G.L., Malmberg R.L., Price R.A.;
RT   "Phylogenetic utility of the nuclear gene arginine decarboxylase: an
RT   example from Brassicaceae.";
RL   Mol. Biol. Evol. 15:1312-1320(1998).
DR   EMBL; AF064654; AAC68593.1; -.
DR   PIR; T12393; T12393.
DR   GO; GO:0009507; C:chloroplast; IEA.
DR   GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR   GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA.
DR   InterPro; IPR003945; NADHpl_oxred5.
DR   InterPro; IPR002128; Oxidored_q1_C.
DR   Pfam; PF01010; Oxidored_q1_C; 1.
DR   PRINTS; PR01435; NPOXDRDTASE5.
KW   Chloroplast.
FT   NON_TER       1      1
FT   NON_TER     260    260
SQ   SEQUENCE   260 AA;  30565 MW;  72E8DA2616AB9CF4 CRC64;

  Query Match             50.6%;  Score 44;  DB 2;  Length 260;
  Best Local Similarity   41.7%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 FHRWSSYMVHWK 14
              | :|:|  :||:
Db        192 FQKWNSKRIHWE 203


RESULT 31
Q8HRN8
ID   Q8HRN8      PRELIMINARY;      PRT;   328 AA.
AC   Q8HRN8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   NADH dehydrogenase subunit F (Fragment).
GN   Name=ndhF;
OS   Arabidopsis thaliana (Mouse-ear cress).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hall J.C., Sytsma K.J., Iltis H.H.;
RT   "Phylogeny of Capparaceae and Brassicaceae based on chloroplast
RT   sequence data.";
RL   Am. J. Bot. 89:1826-1842(2002).
DR   EMBL; AY122394; AAM82798.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
DR   GO; GO:0009523; C:photosystem II; IEA.
DR   GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0042773; P:ATP synthesis coupled electron transport; IEA.
DR   InterPro; IPR003945; NADHpl_oxred5.
DR   InterPro; IPR002128; Oxidored_q1_C.
DR   Pfam; PF01010; Oxidored_q1_C; 1.
DR   PRINTS; PR01435; NPOXDRDTASE5.
KW   Chloroplast.
FT   NON_TER       1      1
FT   NON_TER     328    328
SQ   SEQUENCE   328 AA;  38091 MW;  D762CACB85F262D0 CRC64;

  Query Match             50.6%;  Score 44;  DB 2;  Length 328;
  Best Local Similarity   41.7%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;
```

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Qy          3 FHRWSSYMVHWK 14
              | :|:|  :||:
Db        278 FQKWNSKRIHWE 289


RESULT 32
Q6YT37
ID   Q6YT37      PRELIMINARY;      PRT;   357 AA.
AC   Q6YT37;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Leucine-rich repeat-containing 2.
GN   Name=LRRC2;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP006185; BAD08653.1; -.
DR   InterPro; IPR001611; LRR.
DR   InterPro; IPR003591; LRR_typ.
DR   Pfam; PF00560; LRR_1; 5.
DR   PRINTS; PR00019; LEURICHRPT.
DR   SMART; SM00369; LRR_TYP; 4.
SQ   SEQUENCE   357 AA;  41468 MW;  3DF3C3DF0DE32EF0 CRC64;

  Query Match             50.6%;  Score 44;  DB 2;  Length 357;
  Best Local Similarity   47.4%;  Pred. No. 1.5e+02;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    6;  Gaps    1;

Qy          2 EFHRWSSYMV------HWK 14
              | |:|||  |      |||
Db         93 EGHKWSSEFVFELFGEHWK 111


RESULT 33
Q7S6U0
ID   Q7S6U0      PRELIMINARY;      PRT;   467 AA.
AC   Q7S6U0;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   Name=NCU05499.1;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OR74A;
RA   Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA   Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA   Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA   Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA   Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA   Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA   Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT   "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL   Nature 0:0-0(2003).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABX01000322; EAA31225.1; -.
DR   HSSP; Q93099; 1EYB.
DR   GO; GO:0004411; F:homogentisate 1,2-dioxygenase activity; IEA.
DR   GO; GO:0006559; P:L-phenylalanine catabolism; IEA.
DR   GO; GO:0006570; P:tyrosine metabolism; IEA.
DR   InterPro; IPR005708; HmgA.
DR   InterPro; IPR011051; RmlC_like_cupin.
DR   Pfam; PF04209; HgmA; 1.
DR   TIGRFAMs; TIGR01015; hmgA; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   467 AA;  51560 MW;  21DB84436A32F316 CRC64;

  Query Match             50.6%;  Score 44;  DB 2;  Length 467;
  Best Local Similarity   54.5%;  Pred. No. 2e+02;
  Matches    6;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 HRWSSYMVHWK 14
              | |    ||||
Db        444 HSWGGVKVHWK 454


RESULT 34
NU5C_ARATH
ID   NU5C_ARATH     STANDARD;      PRT;   746 AA.
AC   P56752; Q9MS93;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   NAD(P)H-quinone oxidoreductase chain 5, chloroplast (EC 1.6.5.-)
DE   (NAD(P)H dehydrogenase, chain 5) (NADH-plastoquinone oxidoreductase
DE   chain 5).
GN   Name=ndhF; OrderedLocusNames=AtCg01010;
OS   Arabidopsis thaliana (Mouse-ear cress).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=20039611; PubMed=10574454;
RA   Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
RT   "Complete structure of the chloroplast genome of Arabidopsis
RT   thaliana.";
RL   DNA Res. 6:283-290(1999).
RN   [2]
RP   SEQUENCE OF 18-426 FROM N.A.
RA   Graham S.W., Reeves P.A., Burns A., Olmstead R.G.;
RT   "Long branches in the seed plants and the root of the angiosperms.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: NAD(P)H + plastoquinone = NAD(P)(+) +
CC       plastoquinol.
CC   -!- SIMILARITY: Belongs to the complex I subunit 5 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AP000423; BAA84434.1; -.
DR   EMBL; AF238049; AAF90035.1; -.
DR   InterPro; IPR003945; NADHpl_oxred5.
DR   InterPro; IPR003916; NADHub_oxred5.
DR   InterPro; IPR001750; Oxidored_q1.
DR   InterPro; IPR002128; Oxidored_q1_C.
DR   InterPro; IPR001516; Oxidored_q1_N.
DR   Pfam; PF00361; Oxidored_q1; 1.
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```
DR   Pfam; PF01010; Oxidored_q1_C; 1.
DR   Pfam; PF00662; Oxidored_q1_N; 1.
DR   PRINTS; PR01434; NADHDHGNASE5.
DR   TIGRFAMs; TIGR01974; NDH_I_L; 1.
KW   Chloroplast; NAD; NADP; Oxidoreductase; Plastoquinone; Quinone.
SQ   SEQUENCE   746 AA;  85238 MW;  1391A7875E9E7A29 CRC64;

  Query Match             50.6%;  Score 44;  DB 1;  Length 746;
  Best Local Similarity   41.7%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 FHRWSSYMVHWK 14
              | :|:|  :||:
Db        640 FQKWNSKRIHWE 651


RESULT 35
Q94BA9
ID   Q94BA9      PRELIMINARY;      PRT;   270 AA.
AC   Q94BA9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Maturase K (Fragment).
GN   Name=matK;
OS   Rhagodia baccata (Coastal saltbush).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC   Caryophyllales; Amaranthaceae; Rhagodia.
OX   NCBI_TaxID=169240;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cuenoud P., Savolainen V., Chatrou L.W., Powell M., Grayer R.J.,
RA   Chase M.W.;
RT   "Molecular phylogenetics of Caryophyllales based on nuclear 18S rDNA
RT   and plastid rbcL, atpB, and matK DNA sequences.";
RL   Am. J. Bot. 89:132-144(2002).
DR   EMBL; AY042643; AAK94629.1; -.
DR   GO; GO:0008380; P:RNA splicing; IEA.
DR   InterPro; IPR008998; Agglutinin.
DR   InterPro; IPR000442; Intron_maturse2.
DR   InterPro; IPR002866; MatK_N.
DR   Pfam; PF01348; Intron_maturas2; 1.
DR   Pfam; PF01824; MatK_N; 1.
FT   NON_TER       1      1
FT   NON_TER     270    270
SQ   SEQUENCE   270 AA;  32116 MW;  76375CF8CDC39FD0 CRC64;

  Query Match             50.0%;  Score 43.5;  DB 2;  Length 270;
  Best Local Similarity   41.7%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    5;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          4 HRWSSYMVH-WK 14
              |:| :|::| |:
Db        147 HKWKNYLIHFWQ 158


RESULT 36
Q89Z67
ID   Q89Z67      PRELIMINARY;      PRT;   651 AA.
AC   Q89Z67;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative helicase.
GN   OrderedLocusNames=BT4510;
OS   Bacteroides thetaiotaomicron.
OC   Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC   Bacteroidaceae; Bacteroides.
OX   NCBI_TaxID=818;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VPI-5482 / ATCC 29148;
RX   MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA   Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA   Chiang H.C., Hooper L.V., Gordon J.I.;
RT   "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL   Science 299:2074-2076(2003).
DR   EMBL; AE016945; AAO79615.1; -.
DR   GO; GO:0004386; F:helicase activity; IEA.
DR   InterPro; IPR007936; VirE.
DR   Pfam; PF05272; VirE; 1.
KW   Complete proteome; Helicase.
SQ   SEQUENCE   651 AA;  76145 MW;  58B4682888CB6F0A CRC64;

  Query Match             50.0%;  Score 43.5;  DB 2;  Length 651;
  Best Local Similarity   61.5%;  Pred. No. 3.2e+02;
  Matches    8;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          3 FHRWSSYMV-HWK 14
              ||||   || ||:
Db        387 FHRWFLNMVSHWR 399


RESULT 37
Q8A059
ID   Q8A059      PRELIMINARY;      PRT;   692 AA.
AC   Q8A059;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=BT4162;
OS   Bacteroides thetaiotaomicron.
OC   Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC   Bacteroidaceae; Bacteroides.
OX   NCBI_TaxID=818;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VPI-5482 / ATCC 29148;
RX   MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA   Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA   Chiang H.C., Hooper L.V., Gordon J.I.;
RT   "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL   Science 299:2074-2076(2003).
DR   EMBL; AE016944; AAO79267.1; -.
DR   InterPro; IPR007936; VirE.
DR   Pfam; PF05272; VirE; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   692 AA;  80469 MW;  D3846127234986BB CRC64;

  Query Match             50.0%;  Score 43.5;  DB 2;  Length 692;
  Best Local Similarity   61.5%;  Pred. No. 3.4e+02;
  Matches    8;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          3 FHRWSSYMV-HWK 14
              ||||   || ||:
Db        430 FHRWFLNMVAHWR 442


RESULT 38
Q7MZE7
ID   Q7MZE7      PRELIMINARY;      PRT;   186 AA.
AC   Q7MZE7;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Similar to unknown protein.
GN   OrderedLocusNames=plu4345;
OS   Photorhabdus luminescens (subsp. laumondii).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Photorhabdus.
OX   NCBI_TaxID=141679;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TT01;
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RX   MEDLINE=22957627; PubMed=14528314;
RA   Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA   Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA   Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA   Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA   Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT   "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT   luminescens.";
RL   Nat. Biotechnol. 21:1307-1313(2003).
DR   EMBL; BX571873; CAE16717.1; -.
DR   PhotoList; plu4345; -.
KW   Complete proteome.
SQ   SEQUENCE   186 AA;  21840 MW;  2DA67207F062B276 CRC64;

  Query Match             49.4%;  Score 43;  DB 2;  Length 186;
  Best Local Similarity   54.5%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMV 11
              :|| ||::|:|
Db         71 SEFERWNNYLV 81


RESULT 39
Q853E9
ID   Q853E9      PRELIMINARY;      PRT;   196 AA.
AC   Q853E9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Gp132.
GN   Name=132;
OS   Mycobacteriophage Bxz1.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX   NCBI_TaxID=205877;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22592660; PubMed=12705866; DOI=10.1016/S0092-8674(03)00233-2;
RA   Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
RA   Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
RA   Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,
RA   Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA   Hatfull G.F.;
RT   "Origins of highly mosaic mycobacteriophage genomes.";
RL   Cell 113:171-182(2003).
DR   EMBL; AY129337; AAN16788.1; -.
SQ   SEQUENCE   196 AA;  22038 MW;  506AEC5B64ABCE3C CRC64;

  Query Match             49.4%;  Score 43;  DB 2;  Length 196;
  Best Local Similarity   50.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              :|| : ||:  |||
Db        129 SEFSKLSSFGAHWK 142


RESULT 40
Q96BH3
ID   Q96BH3      PRELIMINARY;      PRT;   223 AA.
AC   Q96BH3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Epididymal sperm binding protein 1.
GN   Name=ELSPBP1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015598; AAH15598.1; -.
DR   HSSP; P02784; 1H8P.
DR   Genew; HGNC:14417; ELSPBP1.
DR   InterPro; IPR000562; FN_Type_II.
DR   Pfam; PF00040; fn2; 4.
DR   PRINTS; PR00013; FNTYPEII.
DR   ProDom; PD000995; FN_Type_II; 3.
DR   SMART; SM00059; FN2; 4.
DR   PROSITE; PS00023; FIBRONECTIN_2; 1.
SQ   SEQUENCE   223 AA;  26105 MW;  F29CCF5BA3E5CE51 CRC64;

  Query Match             49.4%;  Score 43;  DB 2;  Length 223;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 RWSSYMVHW 13
              |||||:: |
Db          3 RWSSYLLGW 11


RESULT 41
Q96RT0
ID   Q96RT0      PRELIMINARY;      PRT;   223 AA.
AC   Q96RT0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Seminal plasma protein-like protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Luo Y., Zhang X., Yu B.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF279147; AAK69481.1; -.
DR   HSSP; P02784; 1H8P.
DR   InterPro; IPR000562; FN_Type_II.
DR   Pfam; PF00040; fn2; 4.
DR   PRINTS; PR00013; FNTYPEII.
DR   ProDom; PD000995; FN_Type_II; 3.
DR   SMART; SM00059; FN2; 4.
DR   PROSITE; PS00023; FIBRONECTIN_2; 1.
SQ   SEQUENCE   223 AA;  26077 MW;  F29CD04BA3E5CE51 CRC64;

  Query Match             49.4%;  Score 43;  DB 2;  Length 223;
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  Best Local Similarity   66.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 RWSSYMVHW 13
              |||||:: |
Db          3 RWSSYLLGW 11


RESULT 42
Q9LMW9
ID   Q9LMW9      PRELIMINARY;      PRT;   392 AA.
AC   Q9LMW9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   F5M15.2.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
RA   Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA   Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
RA   Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA   Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA   Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA   Ecker J.R.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA   Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA   Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA   Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA   Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA   Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA   Theologis A., Ecker J.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC027665; AAF79601.1; -.
DR   InterPro; IPR006527; F_box_assoc_1.
DR   TIGRFAMs; TIGR01640; F_box_assoc_1; 1.
SQ   SEQUENCE   392 AA;  44526 MW;  A8135F563D904EEB CRC64;

  Query Match             49.4%;  Score 43;  DB 2;  Length 392;
  Best Local Similarity   50.0%;  Pred. No. 2.3e+02;
  Matches    9;  Conservative    2;  Mismatches    3;  Indels    4;  Gaps    1;

Qy          1 AEFHRWSSYMV----HWK 14
              || |:||||:      ||
Db        298 AEKHQWSSYIYVLPPPWK 315


RESULT 43
Q9LM89
ID   Q9LM89      PRELIMINARY;      PRT;   422 AA.
AC   Q9LM89;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   F2D10.14.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA   Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA   Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA   Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA   Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA   Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA   Ecker J.R.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Shinn P., Brooks S., Buehler E., Chao Q., Cheuk R., Johnson-Hopson C.,
RA   Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA   Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA   Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA   Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA   Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA   Theologis A., Ecker J.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC069251; AAF80636.1; -.
DR   PIR; D86339; D86339.
DR   InterPro; IPR001810; F-box.
DR   InterPro; IPR006527; F_box_assoc_1.
DR   Pfam; PF00646; F-box; 1.
DR   SMART; SM00256; FBOX; 1.
DR   TIGRFAMs; TIGR01640; F_box_assoc_1; 1.
SQ   SEQUENCE   422 AA;  48016 MW;  7D02BC286346BC52 CRC64;

  Query Match             49.4%;  Score 43;  DB 2;  Length 422;
  Best Local Similarity   50.0%;  Pred. No. 2.5e+02;
  Matches    9;  Conservative    2;  Mismatches    3;  Indels    4;  Gaps    1;

Qy          1 AEFHRWSSYMV----HWK 14
              || |:||||:      ||
Db        328 AEKHQWSSYIYVLPPPWK 345


RESULT 44
SMP3_YEAST
ID   SMP3_YEAST     STANDARD;      PRT;   516 AA.
AC   Q04174; Q99400;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   25-JAN-2005 (Rel. 46, Last annotation update)
DE   SMP3 protein.
GN   Name=SMP3; OrderedLocusNames=YOR149C;
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NBW5;
RX   MEDLINE=91172125; PubMed=2005867;
RA   Irie K., Araki H., Oshima Y.;
RT   "Mutations in a Saccharomyces cerevisiae host showing increased
RT   holding stability of the heterologous plasmid pSR1.";
RL   Mol. Gen. Genet. 225:257-265(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / FY1678;
RX   PubMed=9046089;
RX   DOI=10.1002/(SICI)1097-0061(199701)13:1<73::AID-YEA52>3.3.CO;2-D;
RA   Bordonne R., Camasses A., Madania A., Poch O., Tarassov I., Winsor B.,
RA   Martin R.P.;
RT   "Analysis of a 35.6 kb region on the right arm of Saccharomyces
RT   cerevisiae chromosome XV.";
RL   Yeast 13:73-83(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97313270; PubMed=9169874;
RA   Dujon B., Albermann K., Aldea M., Alexandraki D., Ansorge W.,
RA   Arino J., Benes V., Bohn C., Bolotin-Fukuhara M., Bordonne R.,
RA   Boyer J., Camasses A., Casamayor A., Casas C., Cheret G.,
RA   Cziepluch C., Daignan-Fornier B., Dang D.V., de Haan M., Delius H.,
RA   Durand P., Fairhead C.A., Feldmann H., Gaillon L., Galisson F.,
RA   Gamo F.-J., Gancedo C., Goffeau A., Goulding S.E., Grivell L.A.,
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RA   Habbig B., Hand N.J., Hani J., Hattenhorst U., Hebling U.,
RA   Hernando Y., Herrero E., Heumann K., Hiesel R., Hilger F., Hofmann B.,
RA   Hollenberg C.P., Hughes B., Jauniaux J.-C., Kalogeropoulos A.,
RA   Katsoulou C., Kordes E., Lafuente M.J., Landt O., Louis E.J.,
RA   Maarse A.C., Madania A., Mannhaupt G., Marck C., Martin R.P.,
RA   Mewes H.-W., Michaux G., Paces V., Parle-McDermott A.G., Pearson B.M.,
RA   Perrin A., Pettersson B., Poch O., Pohl T.M., Poirey R.,
RA   Portetelle D., Pujol A., Purnelle B., Ramezani Rad M., Rechmann S.,
RA   Schwager C., Schweizer M., Sor F., Sterky F., Tarassov I.A.,
RA   Teodoru C., Tettelin H., Thierry A., Tobiasch E., Tzermia M.,
RA   Uhlen M., Unseld M., Valens M., Vandenbol M., Vetter I., Vleck C.,
RA   Voet M., Volckaert G., Voss H., Wambutt R., Wedler H., Wiemann S.,
RA   Winsor B., Wolfe K.H., Zollner A., Zumstein E., Kleine K.;
RT   "The nucleotide sequence of Saccharomyces cerevisiae chromosome XV.";
RL   Nature 387:98-102(1997).
CC   -!- FUNCTION: Essential protein involved in plasmid maintenance with
CC       SMP2.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: To S.pombe SpAC4G8.12c.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X58121; CAA41123.1; -.
DR   EMBL; U55020; AAC49635.1; -.
DR   EMBL; Z75057; CAA99355.1; -.
DR   PIR; S67037; S67037.
DR   GermOnline; 143737; -.
DR   SGD; S000005675; SMP3.
DR   GO; GO:0006276; P:plasmid maintenance; IMP.
DR   InterPro; IPR005599; Alg9_trans.
DR   Pfam; PF03901; Glyco_transf_22; 1.
KW   Transmembrane.
FT   TRANSMEM      6     26       Potential.
FT   TRANSMEM     61     81       Potential.
FT   TRANSMEM    176    196       Potential.
FT   TRANSMEM    211    231       Potential.
FT   TRANSMEM    271    291       Potential.
FT   TRANSMEM    296    316       Potential.
FT   TRANSMEM    318    338       Potential.
FT   TRANSMEM    349    369       Potential.
FT   CONFLICT    122    123       MQ -> IK (in Ref. 1).
FT   CONFLICT    163    163       E -> G (in Ref. 1).
FT   CONFLICT    169    169       S -> R (in Ref. 1).
FT   CONFLICT    279    279       V -> L (in Ref. 1).
SQ   SEQUENCE   516 AA;  59900 MW;  8D8404622CB69534 CRC64;

  Query Match             49.4%;  Score 43;  DB 1;  Length 516;
  Best Local Similarity   66.7%;  Pred. No. 3e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 WSSYMVHWK 14
              |  | ||||
Db        204 WKFYRVHWK 212


RESULT 45
Q95TI1
ID   Q95TI1      PRELIMINARY;      PRT;   564 AA.
AC   Q95TI1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   SD02533p.
GN   Name=az2;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA   Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA   Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA   Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY058758; AAL13987.1; -.
DR   FlyBase; FBgn0025185; az2.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   InterPro; IPR000215; Prot_inh_serpin.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF00096; zf-C2H2; 7.
DR   SMART; SM00355; ZnF_C2H2; 7.
DR   PROSITE; PS00284; SERPIN; UNKNOWN_1.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 6.
SQ   SEQUENCE   564 AA;  65530 MW;  15CE998366CE19D6 CRC64;

  Query Match             49.4%;  Score 43;  DB 2;  Length 564;
  Best Local Similarity   53.8%;  Pred. No. 3.3e+02;
  Matches    7;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              || ||  ::|| |
Db          2 EFKRWREFIVHVK 14


Search completed: October 12, 2005, 10:19:56
Job time : 77 secs
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OM protein - protein search, using sw model

Run on: October 12, 2005, 10:06:29 ; Search time 15 Seconds
(without alignments)
89.802 Million cell updates/sec

Title: US-09-155-076-1
Perfect score: 87
Sequence: 1 AEFHRWSSYMVHWK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	87	100.0	583	2	S10712	acetylcholinestera
2	87	100.0	584	2	S48724	acetylcholinestera
3	87	100.0	614	2	A39256	acetylcholinestera
4	87	100.0	614	2	JH0314	acetylcholinestera
5	87	100.0	614	2	JH0811	acetylcholinestera
6	80	92.0	596	1	ACRYE	acetylcholinestera
7	80	92.0	599	1	A38868	acetylcholinestera
8	65	74.7	767	2	S47639	acetylcholinestera
9	62	71.3	602	1	ACHU	cholinesterase (EC
10	61	70.1	581	2	C39768	cholinesterase (EC
11	61	70.1	603	2	S70849	cholinesterase (EC
12	44	50.6	260	2	T12393	NADH2 dehydrogenas
13	43	49.4	422	2	D86339	protein F2D10.14 [
14	43	49.4	516	2	S67037	SMP3 protein - yea
15	42	48.3	100	2	A87273	conserved hypothet
16	42	48.3	1792	2	T08878	supervillin P205 -
17	41	47.1	290	2	C96911	transcription regu
18	41	47.1	397	2	A75137	hypothetical prote
19	41	47.1	512	2	F96741	probable sucrose t
20	41	47.1	523	2	A97177	site-specific reco
21	41	47.1	535	2	B83936	hypothetical prote
22	41	47.1	818	2	H83904	hypothetical prote
23	41	47.1	1323	2	T30253	spalt protein - mo
24	40.5	46.6	510	1	S64059	stearoyl-CoA 9-des
25	40	46.0	90	2	PH1152	Ig heavy chain V r
26	40	46.0	184	2	JC2104	hypothetical 20.8K
27	40	46.0	211	2	B84035	hypothetical prote
28	40	46.0	245	2	S64351	hypothetical prote
29	40	46.0	450	2	A64546	hypothetical prote
30	40	46.0	1350	2	T30341	zinc finger protei
31	40	46.0	1995	2	T08166	probable membrane
32	39.5	45.4	469	2	S74825	probable Rieske ir
33	39.5	45.4	542	2	T02379	hypothetical prote
34	39	44.8	100	2	T09856	sucrose synthase (
35	39	44.8	138	1	HVMST7	Ig heavy chain pre
36	39	44.8	199	2	B82315	hypothetical prote
37	39	44.8	226	2	S37434	membrane glycoprot
38	39	44.8	226	2	D49591	membrane protein M
39	39	44.8	259	2	T12386	NADH2 dehydrogenas
40	39	44.8	260	2	T12395	NADH2 dehydrogenas
41	39	44.8	260	2	T12394	NADH2 dehydrogenas
42	39	44.8	260	2	T14435	NADH2 dehydrogenas
43	39	44.8	272	2	F89904	glycerol uptake fa
44	39	44.8	408	2	D83191	conserved hypothet
45	39	44.8	507	2	B42249	serine-type carbox
46	39	44.8	524	2	T04564	cytochrome P450 ho
47	39	44.8	526	2	T04566	cytochrome P450 ho
48	39	44.8	618	2	S33044	hypothetical prote
49	39	44.8	651	2	F89798	hypothetical prote
50	39	44.8	1237	2	T37529	hypothetical prote
51	38.5	44.3	196	2	AB2265	hypothetical prote
52	38.5	44.3	277	2	G89833	teichoic acid tran
53	38.5	44.3	287	2	T04236	xyloglucan endo-1,
54	38.5	44.3	907	2	AB1885	hypothetical prote
55	38	43.7	58	2	D49038	Ig lambda chain V
56	38	43.7	117	2	S01185	NADH2 dehydrogenas
57	38	43.7	117	2	G25797	NADH2 dehydrogenas
58	38	43.7	119	2	S20640	Ig heavy chain V r
59	38	43.7	122	2	S32185	Ig heavy chain V r
60	38	43.7	157	2	G82214	hypothetical prote
61	38	43.7	166	2	PL0012	Ig heavy chain pre
62	38	43.7	237	2	G90486	hypothetical prote
63	38	43.7	239	2	C97372	hypothetical prote
64	38	43.7	239	2	AB2590	conserved hypothet
65	38	43.7	267	2	B86313	hypothetical prote
66	38	43.7	295	2	E70707	hypothetical prote
67	38	43.7	298	2	AF0578	CitG protein [impo
68	38	43.7	302	2	A95371	probable LysR-fami
69	38	43.7	351	1	SAVZVV	surface antigen pr
70	38	43.7	351	1	SAVZWR	surface antigen pr
71	38	43.7	353	1	SAVZVC	surface antigen pr
72	38	43.7	358	2	AB1746	hypothetical prote
73	38	43.7	379	2	T32778	hypothetical prote
74	38	43.7	591	2	B82429	polyhydroxyalkanoi
75	38	43.7	612	2	F83000	probable two-compo
76	38	43.7	619	2	B87682	hypothetical prote
77	38	43.7	650	2	S23217	beta-fructofuranos
78	38	43.7	710	2	G82689	soluble lytic mure
79	38	43.7	1234	2	A34911	band 3-related pro
80	38	43.7	1237	2	A56764	band 3-related pro
81	38	43.7	1237	2	A31789	band 3-related pro
82	38	43.7	1239	1	A32579	neuroglian - fruit
83	38	43.7	2924	2	T18378	variant-specific s
84	38	43.7	3026	2	T28431	variant surface pr
85	38	43.7	3078	2	T28432	variant-specific s
86	37.5	43.1	285	2	S72787	hypothetical prote
87	37.5	43.1	333	2	S52960	NADH2 dehydrogenas
88	37.5	43.1	494	2	A48285	exopolyphosphatase
89	37.5	43.1	494	2	H91217	guanosine pentapho
90	37.5	43.1	494	2	A86064	guanosine pentapho
91	37	42.5	71	2	PH1136	Ig heavy chain V r
92	37	42.5	96	2	S17606	Ig heavy chain V r
93	37	42.5	97	2	S26895	Ig heavy chain V r
94	37	42.5	109	2	S68171	Ig lambda chain V
95	37	42.5	111	2	S25033	Ig heavy chain V r
96	37	42.5	111	2	S25034	Ig heavy chain V r
97	37	42.5	119	2	S03077	Ig heavy chain V r
98	37	42.5	137	1	G2MS43	Ig heavy chain pre
99	37	42.5	162	2	T17049	NADH2 dehydrogenas
100	37	42.5	162	2	AB1950	hypothetical prote
101	37	42.5	185	2	S48943	hypothetical prote
102	37	42.5	222	2	E95294	conserved hypothet

103	37	42.5	228	2	A83098	hypothetical prote
104	37	42.5	240	2	C87409	hypothetical prote
105	37	42.5	246	2	B97752	hypothetical prote
106	37	42.5	259	2	B72505	hypothetical prote
107	37	42.5	285	2	S55960	probable membrane
108	37	42.5	299	2	AC0794	conserved hypothet
109	37	42.5	321	2	S59388	probable membrane
110	37	42.5	328	1	DEHUE7	estradiol 17beta-d
111	37	42.5	345	2	T24659	hypothetical prote
112	37	42.5	389	2	E90431	sulfolipid biosynt
113	37	42.5	438	2	B71963	probable outer mem
114	37	42.5	499	2	G82891	hypothetical prote
115	37	42.5	506	2	F83545	hypothetical prote
116	37	42.5	552	2	T08148	proline-rich myros
117	37	42.5	662	2	A33481	interferon-induced
118	37	42.5	676	2	T01092	cullin-like protei
119	37	42.5	686	2	S30075	ferric reductase (
120	37	42.5	871	2	T43427	pob1 protein - fis
121	37	42.5	891	2	T29561	hypothetical prote
122	37	42.5	1096	2	C87263	hypothetical prote
123	37	42.5	1332	2	T15670	hypothetical prote
124	37	42.5	1350	2	S00647	finger protein - A
125	37	42.5	1357	2	S57052	hypothetical prote
126	37	42.5	2240	2	T37057	probable multi-dom
127	36.5	42.0	84	2	T51757	hypothetical prote
128	36.5	42.0	125	2	AE0562	probable membrane
129	36.5	42.0	186	2	T50361	hypothetical prote
130	36.5	42.0	290	2	B97100	pyridoxal kinase r
131	36.5	42.0	316	2	T19435	hypothetical prote
132	36.5	42.0	372	2	F70467	hypothetical prote
133	36.5	42.0	1407	2	B42239	adenylate cyclase
134	36	41.4	40	2	S33407	Ig heavy chain V r
135	36	41.4	94	2	PH0996	Ig heavy chain V r
136	36	41.4	96	2	S17617	Ig heavy chain V r
137	36	41.4	96	2	S17618	Ig heavy chain V r
138	36	41.4	97	2	S17603	Ig heavy chain V r
139	36	41.4	98	2	PH1111	Ig heavy chain V r
140	36	41.4	98	2	PH1147	Ig heavy chain V r
141	36	41.4	98	2	S26313	Ig heavy chain V r
142	36	41.4	98	2	S26312	Ig heavy chain V r
143	36	41.4	101	2	S26311	Ig heavy chain V r
144	36	41.4	101	2	S26310	Ig heavy chain V r
145	36	41.4	104	2	S26466	Ig heavy chain V r
146	36	41.4	104	2	PH0991	Ig heavy chain V r
147	36	41.4	106	2	F32513	Ig heavy chain V r
148	36	41.4	109	2	PH0989	Ig heavy chain V r
149	36	41.4	109	2	PH1094	Ig heavy chain V r
150	36	41.4	109	2	PH1096	Ig heavy chain V r
151	36	41.4	110	2	PH0995	Ig heavy chain V r
152	36	41.4	111	2	PH0993	Ig heavy chain V r
153	36	41.4	111	2	PH0994	Ig heavy chain V r
154	36	41.4	111	2	PH0992	Ig heavy chain V r
155	36	41.4	112	2	S26473	Ig heavy chain V r
156	36	41.4	123	2	C87662	IS298, transposase
157	36	41.4	125	2	S20639	Ig heavy chain V r
158	36	41.4	131	2	S66537	Ig heavy chain V r
159	36	41.4	138	2	S21810	Ig heavy chain V r
160	36	41.4	156	2	E84197	hypothetical prote
161	36	41.4	193	2	T34047	hypothetical prote
162	36	41.4	196	2	T29016	hypothetical prote
163	36	41.4	210	2	A82411	probable methyltra
164	36	41.4	214	2	PC4202	monoclonal antibod
165	36	41.4	221	2	T27980	hypothetical prote
166	36	41.4	228	2	D90620	cytochrome c oxida
167	36	41.4	260	2	T12391	NADH2 dehydrogenas
168	36	41.4	260	2	T12387	NADH2 dehydrogenas
169	36	41.4	260	2	T12390	NADH2 dehydrogenas
170	36	41.4	260	2	T12392	NADH2 dehydrogenas
171	36	41.4	272	2	AC1267	glycerol uptake fa
172	36	41.4	272	2	AE1629	glycerol uptake fa
173	36	41.4	276	2	T16523	hypothetical prote
174	36	41.4	288	2	S41194	transmembrane prot
175	36	41.4	308	2	JC5468	leukocidin chain 1
176	36	41.4	326	2	T38706	hypothetical prote
177	36	41.4	396	2	A71134	hypothetical prote
178	36	41.4	397	2	C91007	probable salicylat
179	36	41.4	397	2	E85851	probable hydroxyla
180	36	41.4	410	2	T47926	hypothetical prote
181	36	41.4	475	2	C72538	probable cysteinyl
182	36	41.4	509	2	C84858	probable citrate s
183	36	41.4	516	2	E70779	probable glpD1 pro
184	36	41.4	523	2	T22728	hypothetical prote
185	36	41.4	527	2	H85135	hypothetical prote
186	36	41.4	537	2	F70758	hypothetical prote
187	36	41.4	546	1	C70393	probable adenylyl-
188	36	41.4	570	2	F71049	glutamine-tRNA lig
189	36	41.4	575	1	JC5432	glycoprotein 6-alp
190	36	41.4	578	1	F64578	oligoendopeptidase
191	36	41.4	578	2	B71934	oligopeptidase - H
192	36	41.4	578	2	A35810	alpha,alpha-trehal
193	36	41.4	583	2	JC6504	alpha,alpha-trehal
194	36	41.4	602	2	T22805	hypothetical prote
195	36	41.4	608	2	T22804	hypothetical prote
196	36	41.4	630	1	G64226	hypothetical prote
197	36	41.4	643	2	T33940	hypothetical prote
198	36	41.4	643	2	S55593	membrane protein S
199	36	41.4	654	2	S69673	SAC7 protein - yea
200	36	41.4	669	2	T13335	hypothetical prote
201	36	41.4	669	2	T13640	probable minor str
202	36	41.4	698	2	T21781	hypothetical prote
203	36	41.4	700	2	S09699	bib protein - frui
204	36	41.4	734	1	S26072	photosystem I prot
205	36	41.4	737	2	T06839	probable photosyst
206	36	41.4	751	2	AG1999	(p)ppGpp 3-pyropho
207	36	41.4	755	2	T47806	hypothetical prote
208	36	41.4	758	2	S36711	dolichyl-phosphate
209	36	41.4	758	2	D71072	hypothetical prote
210	36	41.4	765	2	C75100	hypothetical prote
211	36	41.4	766	2	B75059	probable transmemb
212	36	41.4	829	2	S58888	Ins P4-binding pro
213	36	41.4	829	2	S71847	Ins P4-binding pro
214	36	41.4	848	2	T25325	hypothetical prote
215	36	41.4	995	2	H59432	RhoGAP protein hom
216	36	41.4	1117	2	A38227	RNA-splicing regul
217	36	41.4	1256	2	S60461	gene flightless-I
218	36	41.4	1420	2	A32869	apolipoprotein(a)
219	36	41.4	1423	2	A49206	exo-beta-D-fructos
220	36	41.4	4548	1	S00657	apoprotein(a) (EC
221	36	41.4	8243	2	T31307	type I fatty acid
222	35.5	40.8	80	2	C82809	hypothetical prote
223	35.5	40.8	272	2	AB3430	transposase BMEI14
224	35.5	40.8	278	2	AG2176	hypothetical prote
225	35.5	40.8	406	2	AG0548	probable ABC-trans
226	35.5	40.8	411	2	S46800	LAG1 protein - yea
227	35.5	40.8	412	2	F69796	sugar-binding prot
228	35.5	40.8	418	2	S30134	hypothetical prote
229	35.5	40.8	493	2	AH0922	guanosine-5'-triph
230	35.5	40.8	515	2	F88618	protein W06F12.2 [
231	35.5	40.8	562	2	T26242	hypothetical prote
232	35.5	40.8	568	2	T26243	hypothetical prote
233	35.5	40.8	1074	2	G96504	probable En/Spm-li
234	35.5	40.8	1121	2	F86485	hypothetical prote
235	35.5	40.8	1426	2	E90456	oxydoreductase, pr
236	35	40.2	35	2	S46472	Ig heavy chain V r
237	35	40.2	35	2	S26887	Ig heavy chain V r
238	35	40.2	35	2	S46473	Ig heavy chain V r
239	35	40.2	94	2	S20653	Ig heavy chain V r
240	35	40.2	94	2	S20650	Ig heavy chain V r
241	35	40.2	94	2	PL0120	Ig heavy chain V-I
242	35	40.2	96	2	C33730	Ig kappa chain V r
243	35	40.2	97	2	S26885	Ig heavy chain V r
244	35	40.2	97	2	S26886	Ig heavy chain V r
245	35	40.2	97	2	S54855	Ig heavy chain V r
246	35	40.2	98	2	PL0121	Ig heavy chain V-I
247	35	40.2	98	2	S29545	Ig heavy chain V r
248	35	40.2	98	2	S29546	Ig heavy chain V r

249	35	40.2	98	2	S26896	Ig heavy chain V r
250	35	40.2	98	2	PH1061	Ig light chain V r
251	35	40.2	99	2	C48223	Ig heavy chain V r
252	35	40.2	101	2	PH1021	Ig heavy chain V r
253	35	40.2	105	2	PH1020	Ig heavy chain V r
254	35	40.2	109	2	PH1653	Ig heavy chain V r
255	35	40.2	109	2	PH1646	Ig heavy chain V r
256	35	40.2	109	2	PH1644	Ig heavy chain V r
257	35	40.2	111	2	PH1019	Ig heavy chain V r
258	35	40.2	111	2	PH1645	Ig heavy chain V r
259	35	40.2	111	2	S69475	hypothetical prote
260	35	40.2	112	2	PH1022	Ig heavy chain V r
261	35	40.2	114	2	S46390	Ig heavy chain V r
262	35	40.2	114	2	S46391	Ig heavy chain V r
263	35	40.2	114	2	S46392	Ig heavy chain V r
264	35	40.2	114	2	S20707	Ig heavy chain V r
265	35	40.2	116	2	S12557	Ig heavy chain - h
266	35	40.2	116	2	S22558	Ig heavy chain V r
267	35	40.2	117	2	S36270	Ig heavy chain V r
268	35	40.2	118	2	S31677	Ig heavy chain V r
269	35	40.2	118	2	S38717	Ig heavy chain V r
270	35	40.2	119	2	F36005	Ig heavy chain V r
271	35	40.2	120	2	S31112	Ig heavy chain - h
272	35	40.2	121	2	S20783	Ig heavy chain V r
273	35	40.2	121	2	G36005	Ig heavy chain V r
274	35	40.2	122	2	E36005	Ig heavy chain V r
275	35	40.2	123	2	S38493	Ig heavy chain - h
276	35	40.2	134	2	S31679	Ig heavy chain V r
277	35	40.2	137	2	S31701	Ig heavy chain V r
278	35	40.2	160	2	T17048	NADH2 dehydrogenas
279	35	40.2	169	2	D84027	molybdopterin-guan
280	35	40.2	212	2	D64662	biotin operon repr
281	35	40.2	215	2	E84078	hypothetical prote
282	35	40.2	224	2	AD3278	nicotinamide-nucle
283	35	40.2	225	2	A88991	protein C36C5.3 [i
284	35	40.2	235	1	VHVULV	nucleoprotein N -
285	35	40.2	235	1	VHVUNH	nucleoprotein N -
286	35	40.2	250	2	F75219	hypothetical prote
287	35	40.2	255	2	T24406	hypothetical prote
288	35	40.2	259	2	T15841	hypothetical prote
289	35	40.2	264	2	I39696	beta-lactamase (EC
290	35	40.2	268	2	F86678	sugar hydrolase [i
291	35	40.2	279	2	T16816	hypothetical prote
292	35	40.2	279	2	T16425	hypothetical prote
293	35	40.2	279	2	T15313	hypothetical prote
294	35	40.2	297	2	T24718	hypothetical prote
295	35	40.2	299	2	A70713	hypothetical prote
296	35	40.2	304	2	T34475	hypothetical prote
297	35	40.2	318	2	JC6115	gamma-glutamyl hyd
298	35	40.2	319	2	D89778	hypothetical prote
299	35	40.2	325	2	T31989	hypothetical prote
300	35	40.2	330	2	S53990	DNA methyltransfer
301	35	40.2	336	2	C71964	UDP-3-O-[3-hydroxy
302	35	40.2	336	2	D64544	UDP-3-O-[3-hydroxy
303	35	40.2	355	2	C96007	probable ornithine
304	35	40.2	359	2	AE0541	probable fimbrail
305	35	40.2	373	2	A55718	interleukin-2 rece
306	35	40.2	377	2	S60478	probable 1-acyl-sn
307	35	40.2	388	2	F83738	hypothetical prote
308	35	40.2	389	2	C82130	conserved hypothet
309	35	40.2	393	2	T12492	hypothetical prote
310	35	40.2	397	2	F70001	multidrug resistan
311	35	40.2	415	2	B84544	probable WD-40 rep
312	35	40.2	448	2	T15589	hypothetical prote
313	35	40.2	449	2	JQ0172	tubulin beta chain
314	35	40.2	457	2	JQ2184	hypothetical 50.4K
315	35	40.2	466	2	F85913	hypothetical prote
316	35	40.2	466	2	D91069	hypothetical prote
317	35	40.2	466	2	H65045	gamma-aminobutyrat
318	35	40.2	471	2	T34956	probable UDP-N-ace
319	35	40.2	494	2	T09289	nicotinic acetylch
320	35	40.2	494	2	S22324	replication initia
321	35	40.2	516	2	S53007	citrate synthase -
322	35	40.2	527	2	T25131	hypothetical prote
323	35	40.2	529	1	SAHU4F	cell surface antig
324	35	40.2	533	2	T10216	hypothetical prote
325	35	40.2	549	1	S39533	phosphoprotein pho
326	35	40.2	553	2	A88495	protein C06E8.4 [i
327	35	40.2	553	2	H88671	protein F28E10.3 [
328	35	40.2	553	2	T32344	hypothetical prote
329	35	40.2	553	2	T21233	hypothetical prote
330	35	40.2	553	2	T24639	hypothetical prote
331	35	40.2	553	2	A89723	protein F47C8.1 [i
332	35	40.2	555	2	S27163	alpha,alpha-trehal
333	35	40.2	560	2	E96554	hypothetical prote
334	35	40.2	562	2	G70180	serine/threonine k
335	35	40.2	575	2	AG2566	hypothetical prote
336	35	40.2	585	2	T18885	hypothetical prote
337	35	40.2	589	2	I38598	zinc finger protei
338	35	40.2	594	2	T22072	hypothetical prote
339	35	40.2	596	2	T23084	hypothetical prote
340	35	40.2	607	2	T23085	hypothetical prote
341	35	40.2	625	2	S68633	hypothetical prote
342	35	40.2	625	2	T32739	hypothetical prote
343	35	40.2	626	2	AE0123	probable antigenic
344	35	40.2	629	2	T22066	hypothetical prote
345	35	40.2	633	2	T21779	hypothetical prote
346	35	40.2	634	2	S77096	icfG protein slr18
347	35	40.2	637	2	H96592	probable multispan
348	35	40.2	639	2	T50793	hypothetical prote
349	35	40.2	644	2	T22067	hypothetical prote
350	35	40.2	649	2	H86920	probable membrane
351	35	40.2	658	2	T32893	hypothetical prote
352	35	40.2	659	2	D84633	probable multispan
353	35	40.2	661	2	T20877	hypothetical prote
354	35	40.2	662	2	T44219	hypothetical prote
355	35	40.2	662	2	T31986	hypothetical prote
356	35	40.2	669	2	T24571	hypothetical prote
357	35	40.2	670	2	T09205	hypothetical prote
358	35	40.2	670	2	T09274	hypothetical prote
359	35	40.2	670	2	T32221	hypothetical prote
360	35	40.2	671	2	B75607	conserved hypothet
361	35	40.2	677	2	T23083	hypothetical prote
362	35	40.2	682	2	T22064	hypothetical prote
363	35	40.2	685	2	T32571	hypothetical prote
364	35	40.2	689	2	T25202	hypothetical prote
365	35	40.2	692	2	T28783	hypothetical prote
366	35	40.2	695	2	T28782	hypothetical prote
367	35	40.2	699	2	A82425	helicase IV VCA071
368	35	40.2	734	2	T07280	photosystem I P700
369	35	40.2	735	2	S41481	P700 chlorophyll a
370	35	40.2	761	2	H84950	ribonucleoside-dip
371	35	40.2	775	2	T22200	hypothetical prote
372	35	40.2	780	2	T39057	hypothetical prote
373	35	40.2	790	2	T24354	hypothetical prote
374	35	40.2	805	2	C87861	protein F43G9.7 [i
375	35	40.2	805	2	T32377	hypothetical prote
376	35	40.2	815	2	T00264	high carbon dioxid
377	35	40.2	838	2	B38656	vacuolar proton pu
378	35	40.2	874	2	H86167	hypothetical prote
379	35	40.2	891	2	T28828	hypothetical prote
380	35	40.2	919	2	T21049	hypothetical prote
381	35	40.2	1013	2	T16244	hypothetical prote
382	35	40.2	1025	2	H86250	hypothetical prote
383	35	40.2	1050	2	G70396	cation efflux syst
384	35	40.2	1174	2	H84982	exodeoxyribonuclea
385	35	40.2	1188	2	S48861	gene el protein -
386	35	40.2	1227	2	A33638	erythrocyte anion
387	35	40.2	1227	2	B34911	band 3-related pro
388	35	40.2	1232	2	I38496	anion exchanger 3
389	35	40.2	1319	2	H84542	hypothetical prote
390	35	40.2	1458	1	A49707	phospholipase A2 r
391	35	40.2	1463	2	A53210	phospholipase A2 r
392	35	40.2	1493	2	F70435	glutamate synthase
393	35	40.2	2025	2	T21588	hypothetical prote
394	35	40.2	2228	2	T14029	variant-specific s

395	35	40.2	2284	1	GNVVGV	genome polyprotein
396	35	40.2	2405	2	T08164	dynein alpha heavy
397	35	40.2	3335	2	H81702	adherence factor T
398	35	40.2	5107	2	T29144	partial CDS - Caen
399	34.5	39.7	103	2	T05290	hypothetical prote
400	34.5	39.7	123	2	S30529	Ig heavy chain V r
401	34.5	39.7	208	2	T43385	60S ribosomal prot
402	34.5	39.7	309	1	EUSMAG	agarase (EC 3.2.1.
403	34.5	39.7	430	2	E86188	hypothetical prote
404	34.5	39.7	491	2	S06762	beta-galactosidase
405	34.5	39.7	623	1	VGBE68	glycoprotein E - h
406	34.5	39.7	956	2	H75536	2-oxoglutarate deh
407	34.5	39.7	1104	2	T49735	related to MDM1 pr
408	34	39.1	69	2	D25150	Ig heavy chain V r
409	34	39.1	76	2	PH1153	Ig heavy chain V r
410	34	39.1	80	2	F28833	Ig kappa chain V r
411	34	39.1	86	2	A25150	Ig heavy chain V r
412	34	39.1	94	2	S42185	Ig gamma chain V r
413	34	39.1	94	2	PH1142	Ig heavy chain V r
414	34	39.1	94	2	JL0078	Ig heavy chain V r
415	34	39.1	96	2	S17621	Ig heavy chain V r
416	34	39.1	96	2	S17230	Ig heavy chain V r
417	34	39.1	96	2	S17612	Ig heavy chain V r
418	34	39.1	96	2	S17620	Ig heavy chain V r
419	34	39.1	96	2	S17616	Ig heavy chain V r
420	34	39.1	96	2	S17609	Ig heavy chain V r
421	34	39.1	97	2	PH1137	Ig heavy chain V r
422	34	39.1	98	2	S26920	Ig heavy chain V r
423	34	39.1	98	2	PH1164	Ig heavy chain V r
424	34	39.1	98	2	PH1138	Ig heavy chain V r
425	34	39.1	98	2	PH1154	Ig heavy chain V r
426	34	39.1	98	2	PH1118	Ig heavy chain V r
427	34	39.1	98	2	PH1139	Ig heavy chain V r
428	34	39.1	98	2	PH1150	Ig heavy chain V r
429	34	39.1	98	2	PH1156	Ig heavy chain V r
430	34	39.1	98	2	PH1125	Ig heavy chain V r
431	34	39.1	98	2	PH1134	Ig heavy chain V r
432	34	39.1	98	2	PH1105	Ig heavy chain V r
433	34	39.1	98	2	PH1126	Ig heavy chain V r
434	34	39.1	98	2	PH1108	Ig heavy chain V r
435	34	39.1	98	2	PH1119	Ig heavy chain V r
436	34	39.1	98	2	PH1149	Ig heavy chain V r
437	34	39.1	98	2	PH1157	Ig heavy chain V r
438	34	39.1	98	2	PH1114	Ig heavy chain V r
439	34	39.1	98	2	I28833	Ig kappa chain V r
440	34	39.1	98	2	PH1131	Ig heavy chain V r
441	34	39.1	102	2	S26471	Ig heavy chain V r
442	34	39.1	102	2	D83896	potassium channel
443	34	39.1	104	2	PH1665	Ig heavy chain V r
444	34	39.1	108	2	PH1651	Ig heavy chain V r
445	34	39.1	108	2	PH0985	Ig heavy chain V r
446	34	39.1	109	2	S25038	Ig heavy chain V r
447	34	39.1	110	2	S25028	Ig heavy chain V r
448	34	39.1	110	2	E82781	hypothetical prote
449	34	39.1	111	2	S25024	Ig heavy chain V r
450	34	39.1	111	2	S25032	Ig heavy chain V r
451	34	39.1	111	2	S25047	Ig heavy chain V r
452	34	39.1	111	2	S25055	Ig heavy chain V r
453	34	39.1	111	2	S25045	Ig heavy chain V r
454	34	39.1	111	2	S25054	Ig heavy chain V r
455	34	39.1	111	2	S25048	Ig heavy chain V r
456	34	39.1	111	2	S25052	Ig heavy chain V r
457	34	39.1	111	2	S25040	Ig heavy chain V r
458	34	39.1	111	2	S25051	Ig heavy chain V r
459	34	39.1	111	2	S54831	hypothetical prote
460	34	39.1	113	2	S25044	Ig heavy chain V r
461	34	39.1	113	2	S25041	Ig heavy chain V r
462	34	39.1	114	2	PH1667	Ig heavy chain V r
463	34	39.1	115	2	S36284	Ig heavy chain V r
464	34	39.1	115	2	S03527	Ig heavy chain pre
465	34	39.1	115	2	C27563	Ig heavy chain V r
466	34	39.1	116	2	F86676	hypothetical prote
467	34	39.1	116	2	I84704	gene VH104B protei
468	34	39.1	116	2	S26309	Ig heavy chain V r
469	34	39.1	117	1	HVHUHG	Ig heavy chain pre
470	34	39.1	117	1	HVMS02	Ig heavy chain pre
471	34	39.1	117	1	HVMS23	Ig heavy chain pre
472	34	39.1	117	1	HVMS45	Ig heavy chain pre
473	34	39.1	117	1	HVMS61	Ig heavy chain pre
474	34	39.1	117	1	MHMSB4	Ig heavy chain pre
475	34	39.1	117	2	T11356	NADH2 dehydrogenas
476	34	39.1	117	2	S18552	Ig heavy chain V r
477	34	39.1	117	2	S31680	Ig heavy chain V r
478	34	39.1	117	2	S18553	Ig heavy chain V r
479	34	39.1	117	2	JC2269	PL7-6 antibody hea
480	34	39.1	117	2	S55541	Ig heavy chain V r
481	34	39.1	118	2	PH1666	Ig heavy chain V r
482	34	39.1	120	1	MHMS15	Ig heavy chain V r
483	34	39.1	120	2	PH1650	Ig heavy chain V r
484	34	39.1	120	2	S25175	Ig heavy chain V r
485	34	39.1	120	2	S41394	Ig heavy chain V r
486	34	39.1	120	2	B22769	Ig heavy chain V r
487	34	39.1	126	2	S58121	Ig heavy chain V r
488	34	39.1	126	2	S31930	Ig gamma chain pre
489	34	39.1	131	2	A27472	Ig heavy chain pre
490	34	39.1	132	2	AC0780	probable membrane
491	34	39.1	135	2	JQ1225	UncI protein homol
492	34	39.1	136	2	JL0077	Ig heavy chain pre
493	34	39.1	139	1	MHMS18	Ig heavy chain pre
494	34	39.1	141	2	JL0076	Ig heavy chain pre
495	34	39.1	142	2	T36147	probable regulator
496	34	39.1	150	2	C86754	prophage pi2 prote
497	34	39.1	160	2	H86149	protein T1N6.23 [i
498	34	39.1	170	2	B97811	proline/betaine tr
499	34	39.1	174	2	G72381	hypothetical prote
500	34	39.1	179	2	T51570	hypothetical prote

ALIGNMENTS

RESULT 1
S10712
acetylcholinesterase (EC 3.1.1.7) - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 12-May-1995
C;Accession: S10712; A39734; B39734; B25650
R;Doctor, B.P.; Chapman, T.C.; Christner, C.E.; Deal, C.D.; de la Hoz, D.M.; Gentry, M.K
FEBS Lett. 266, 123-127, 1990
A;Title: Complete amino acid sequence of fetal bovine serum acetylcholinesterase and its
A;Reference number: S10712; MUID:90306335; PMID:2365060
A;Accession: S10712
A;Molecule type: protein
A;Residues: 1-583 <DOC>
A;Experimental source: fetal serum
R;Roberts, W.L.; Doctor, B.P.; Foster, J.D.; Rosenberry, T.L.
J. Biol. Chem. 266, 7481-7487, 1991
A;Title: Bovine brain acetylcholinesterase primary sequence involved in intersubunit dis
A;Reference number: A39734; MUID:91210255; PMID:2019579
A;Accession: A39734
A;Molecule type: protein
A;Residues: 1-15,'R',17-38;225-235,'X',237-244;248-264,'X',266-273;365-380;396-404,'X',4
A;Experimental source: brain, erythrocyte
A;Accession: B39734
A;Molecule type: protein
A;Residues: 1-38 <RO2>
A;Experimental source: fetal serum
R;Bon, S.; Chang, J.Y.; Strosberg, A.D.
FEBS Lett. 209, 206-212, 1986
A;Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-solu
inesterase.
A;Reference number: A91370; MUID:87080761; PMID:3792544
A;Accession: B25650
A;Molecule type: protein
A;Residues: 'XS',3-12 <BON>
A;Experimental source: caudate nucleus

C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F;32-538/Domain: cholinesterase homology <CHE>
F;61,265,350,464,541/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;203/Active site: Ser #status predicted

Query Match 100.0%; Score 87; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 555 AEFHRWSSYMVHWK 568

RESULT 2
S48724
acetylcholinesterase - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 14-Nov-1997
C;Accession: S48724
R;Jbilo, O.; L'Hermite, Y.; Talesa, V.; Toutant, J.P.; Chatonnet, A.
Eur. J. Biochem. 225, 115-124, 1994
A;Title: Acetylcholinesterase and butyrylcholinesterase expression in adult rabbit tissu
A;Reference number: S48724; MUID:95010096; PMID:7925428
A;Accession: S48724
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-584 <JBI>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: glycoprotein
F;32-539/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 87; DB 2; Length 584;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
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Db 556 AEFHRWSSYMVHWK 569

RESULT 3
A39256
acetylcholinesterase (EC 3.1.1.7) precursor, brain splice form - human
C;Species: Homo sapiens (man)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 09-Jul-2004
C;Accession: A39256; S03959
R;Soreq, H.; Ben-Aziz, R.; Prody, C.A.; Seidman, S.; Gnatt, A.; Neville, L.; Lieman-Hurw
Proc. Natl. Acad. Sci. U.S.A. 87, 9688-9692, 1990
A;Title: Molecular cloning and construction of the coding region for human acetylcholine
A;Reference number: A39256; MUID:91088577; PMID:2263619
A;Accession: A39256
A;Molecule type: mRNA; DNA
A;Residues: 1-614 <SOR>
A;Cross-references: UNIPROT:P22303; GB:M55040; NID:g177974; PIDN:AAA68151.1; PID:g177975
A;Note: this sequence represents composite of clones including clone ABGACHE from adult
nce should represent an authentic brain splice form
R;Chhajlani, V.; Derr, D.; Earles, B.; Schmell, E.; August, T.
FEBS Lett. 247, 279-282, 1989
A;Title: Purification and partial amino acid sequence analysis of human erythrocyte acet
A;Reference number: S03959; MUID:89232136; PMID:2714437
A;Accession: S03959
A;Molecule type: protein
A;Residues: 256-266,'Y',268-273;306-308,'X',310-313,'X',315-316,'D',318-323,'D',325-326;
Y',532-551 <CHH>
A;Experimental source: erythrocytes
A;Note: this form was a disulfide-linked homodimer
C;Genetics:
A;Gene: GDB:ACHE; YT
A;Cross-references: GDB:118746; OMIM:100740
A;Map position: 7q22-7q22
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; phosphatidyl
F;63-569/Domain: cholinesterase homology <CHE>

Query Match 100.0%; Score 87; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 586 AEFHRWSSYMVHWK 599

RESULT 4
JH0314
acetylcholinesterase (EC 3.1.1.7) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JH0314
R;Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990
A;Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alterna
A;Reference number: JH0314; MUID:90380429; PMID:2400605
A;Accession: JH0314
A;Molecule type: mRNA
A;Residues: 1-614 <RAC>
A;Cross-references: UNIPROT:P21836; EMBL:X56518; NID:g49844; PIDN:CAA39867.1; PID:g49845
A;Experimental source: brain
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-614/Product: acetylcholinesterase #status predicted <MAT>
F;63-569/Domain: cholinesterase homology <CHE>
F;100-127,288-303,440-560/Disulfide bonds: #status predicted
F;234/Active site: Ser #status predicted
F;296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 87; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 586 AEFHRWSSYMVHWK 599

RESULT 5
JH0811
acetylcholinesterase (EC 3.1.1.7) catalytic chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: JH0811
R;Legay, C.; Bon, S.; Vernier, P.; Coussen, F.; Massoulie, J.
J. Neurochem. 60, 337-346, 1993
A;Title: Cloning and expression of a rat acetylcholinesterase subunit: generation of mul
A;Reference number: JH0811; MUID:93107932; PMID:8417155
A;Accession: JH0811
A;Molecule type: mRNA
A;Residues: 1-614 <LEG>
A;Cross-references: UNIPROT:P37136; GB:S50879; NID:g262092; PIDN:AAB24586.1; PID:g262093
A;Experimental source: striatum
C;Comment: This protein is responsible for hydrolysis of acetylcholine at cholinergic sy
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein; muscle; nerve; n
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-614/Product: acetylcholinesterase catalytic chain #status predicted <MAT>
F;63-569/Domain: cholinesterase homology <CHE>
F;100-127,288-303,440-560/Disulfide bonds: #status predicted
F;234,365,478/Active site: Ser, Glu, His #status predicted
F;296,381,495/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 87; DB 2; Length 614;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599
```

RESULT 6
ACRYE
acetylcholinesterase (EC 3.1.1.7) precursor, 11S form [validated] - Pacific electric ray
N;Alternate names: acetylcholinesterase, asymmetric form
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 17-Mar-1987 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: A00773; A60820; A31962; B31962; A23902; B41117; S15677
R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; F
Nature 319, 407-409, 1986
A;Title: Primary structure of Torpedo californica acetylcholinesterase deduced from its
A;Reference number: A00773; MUID:86118676; PMID:3753747
A;Accession: A00773
A;Molecule type: mRNA
A;Residues: 'NS',11-596 <SCH>
A;Cross-references: UNIPROT:P04058; GB:X03439; NID:g64389
A;Experimental source: electric organ
A;Note: parts of this sequence, including the amino and carboxyl ends of the mature prot
R;Schumacher, M.; Camp, S.; Maulet, Y.; Newton, M.; MacPhee-Quigley, K.; Taylor, S.S.; F
Fed. Proc. 45, 2976-2981, 1986
A;Title: Primary structure of acetylcholinesterase: implications for regulation and func
A;Reference number: A60820; MUID:87054662; PMID:3536598
A;Accession: A60820
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 22-596 <SC2>
R;Schumacher, M.; Maulet, Y.; Camp, S.; Taylor, P.
J. Biol. Chem. 263, 18979-18987, 1988
A;Title: Multiple messenger RNA species give rise to the structural diversity in acetylc
A;Reference number: A92701; MUID:89066695; PMID:3198606
A;Accession: A31962
A;Molecule type: mRNA
A;Residues: 1-23 <SC3>
A;Cross-references: EMBL:X03439; NID:g64389
A;Experimental source: clones AChE-11 and AChE-18
A;Note: revision to sequence A00773
A;Accession: B31962
A;Molecule type: DNA; mRNA
A;Residues: 499-565 <SC4>
A;Cross-references: GB:X03439; NID:g64389
A;Experimental source: clone AChE-1
R;MacPhee-Quigley, K.; Taylor, P.; Taylor, S.
J. Biol. Chem. 260, 12185-12189, 1985
A;Title: Primary structures of the catalytic subunits from two molecular forms of acetyl
A;Reference number: A23902; MUID:86008285; PMID:3900071
A;Accession: A23902
A;Molecule type: protein
A;Residues: 22,'B',24-45;214-237 <MAC>
A;Note: active site Ser identification
R;Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo a
A;Reference number: A41117; MUID:91296772; PMID:2068091
A;Accession: B41117
A;Molecule type: protein
A;Residues: 100-108 <KRE>
A;Note: substrate binding site
R;Maulet, Y.; Camp, S.; Gibney, G.; Rachinsky, T.L.; Ekstroem, T.J.; Taylor, P.
Neuron 4, 289-301, 1990
A;Title: Single gene encodes glycophospholipid-anchored and asymmetric acetylcholinester
A;Reference number: PS0113; MUID:90166618; PMID:2306366
A;Accession: S15677
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 557-596 <MAU>
A;Cross-references: EMBL:X56516
R;MacPhee-Quigley, K.; Vedvick, T.S.; Taylor, P.; Taylor, S.S.
J. Biol. Chem. 261, 13565-13570, 1986
A;Title: Profile of the disulfide bonds in acetylcholinesterase.
A;Reference number: A43099; MUID:87008586; PMID:3759980
A;Contents: annotation; disulfide bonds
R;Sussman, J.L.; Harel, M.; Silman, I.
submitted to the Brookhaven Protein Data Bank, October 1991
A;Reference number: A50061; PDB:1ACE
A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481,511-555 of
R;Sussman, J.L.; Harel, M.; Frolow, F.; Oefner, C.; Goldman, A.; Toker, L.; Silman, I.
Science 253, 872-879, 1991
A;Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic
A;Reference number: A43098; MUID:91343928; PMID:1678899
A;Contents: annotation; X-ray crystallography, 2.8 angstroms, residues 26-481,511-555 of
C;Comment: Synapses usually contain this 11S (asymmetric) form of cholinesterase with a
holinesterase occurs on the outer surfaces of cell membranes, including those of erythro
C;Complex: 11S form is disulfide linked homodimer; 18S form is homotetramer, a dimer of
C;Function:
A;Description: hydrolyzes acetylcholine to choline and acetate
A;Pathway: neurotransmitter degradation
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane pro
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-596/Product: acetylcholinesterase, 11S form #status experimental <MAT>
F;51-551/Domain: cholinesterase homology <CHE>
F;80,478,554/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;88-115,275-286,423-542/Disulfide bonds: #status experimental
F;105/Binding site: substrate (Trp) #status experimental
F;221/Active site: Ser #status experimental
F;348,461/Active site: Glu, His #status predicted
F;437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;593/Disulfide bonds: interchain #status experimental

  Query Match   92.0%; Score 80; DB 1; Length 596;
  Best Local Similarity   92.3%; Pred. No. 0.00011;
  Matches   12; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

```
Qy          2 EFHRWSSYMVHWK 14
              |||||||||:|||
Db        569 EFHRWSSYMMHWK 581
```

RESULT 7
A38868
acetylcholinesterase (EC 3.1.1.7) precursor - marbled electric ray
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 23-Apr-1993 #sequence_revision 15-Nov-1996 #text_change 09-Jul-2004
C;Accession: A38868; A29682; S15696; A25650
R;Massoulie, J.; Bon, S.
submitted to the EMBL Data Library, June 1992
A;Reference number: A38868
A;Accession: A38868
A;Molecule type: mRNA
A;Residues: 1-599 <MAS>
A;Cross-references: UNIPROT:P07692; EMBL:X05497; NID:g64414; PIDN:CAA29047.1; PID:g64415
R;Sikorav, J.L.; Krejci, E.; Massoulie, J.
EMBO J. 6, 1865-1873, 1987
A;Title: cDNA sequences of Torpedo marmorata acetylcholinesterase: primary structure of
A;Reference number: A29682; MUID:88004392; PMID:2820709
A;Accession: A29682
A;Molecule type: mRNA
A;Residues: 1-40,'G',42-226,'G',228-272,'G',274-284,'E',286-420,'N',422-599 <SIK>
A;Cross-references: EMBL:X05497
R;Sikorav, J.L.; Duval, N.; Anselmet, A.; Bon, S.; Krejci, E.; Legay, C.; Osterlund, M.;
EMBO J. 7, 2983-2993, 1988
A;Title: Complex alternative splicing of acetylcholinesterase transcripts in Torpedo ele
A;Reference number: S01293; MUID:89030590; PMID:3181125
A;Accession: S15696
A;Molecule type: mRNA
A;Residues: 526-599 <SI2>
A;Cross-references: EMBL:X13172; NID:g64416; PIDN:CAA31570.1; PID:g64417
A;Experimental source: clone pAChE2
R;Bon, S.; Chang, J.Y.; Strosberg, A.D.
FEBS Lett. 209, 206-212, 1986
A;Title: Identical N-terminal peptide sequences of asymmetric forms and of low-salt-solu

```
inesterase.
A;Reference number: A91370; MUID:87080761; PMID:3792544
A;Accession: A25650
A;Molecule type: protein
A;Residues: 25-40,'G',42-47 <BON>
C;Genetics:
A;Gene: AChE
C;Function:
A;Description: hydrolyzes acetylcholine to choline and acetate
A;Pathway: neurotransmitter degradation
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; neurotransmi
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-599/Product: acetylcholinesterase #status predicted <MAT>
F;54-554/Domain: cholinesterase homology <CHE>
F;83,440,481,557/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;91-118,278-289,426-545/Disulfide bonds: #status predicted
F;224,351,464/Active site: Ser, Glu, His #status predicted
F;596/Disulfide bonds: interchain #status predicted

  Query Match             92.0%;  Score 80;  DB 1;  Length 599;
  Best Local Similarity   92.3%;  Pred. No. 0.00011;
  Matches   12;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              |||||||||:|||
Db        572 EFHRWSSYMMHWK 584


RESULT 8
S47639
acetylcholinesterase (EC 3.1.1.7) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S47639
R;Randall, W.R.; Rimer, M.; Gough, N.R.
Biochim. Biophys. Acta 1218, 453-456, 1994
A;Title: Cloning and analysis of chicken acetylcholinesterase transcripts from muscle an
A;Reference number: S47639; MUID:94325359; PMID:8049273
A;Accession: S47639
A;Molecule type: mRNA
A;Residues: 1-767 <RAN>
A;Cross-references: UNIPROT:P36196; EMBL:U03472; NID:g623031; PIDN:AAA60456.1; PID:g4241
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase

  Query Match             74.7%;  Score 65;  DB 2;  Length 767;
  Best Local Similarity   76.9%;  Pred. No. 0.027;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              |||||||||  |:
Db        740 EFHRWSSYMGRWR 752


RESULT 9
ACHU
cholinesterase (EC 3.1.1.8) precursor [validated] - human
N;Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase II
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: A33769; A26613; A33887; A34668; A00772
R;Arpagaus, M.; Kott, M.; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockridge, O.
Biochemistry 29, 124-131, 1990
A;Title: Structure of the gene for human butyrylcholinesterase. Evidence for a single co
A;Reference number: A33769; MUID:90212557; PMID:2322535
A;Accession: A33769
A;Molecule type: DNA
A;Residues: 'MSVQSNLQAGAAAASCISPKYYMIFTPCKLCHLCCRESEIN',1-602 <ARP>
A;Cross-references: UNIPROT:P06276; GB:M32391; GB:J02879
A;Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra
R;Prody, C.A.; Zevin-Sonkin, D.; Gnatt, A.; Goldberg, O.; Soreq, H.
Proc. Natl. Acad. Sci. U.S.A. 84, 3555-3559, 1987
A;Title: Isolation and characterization of full-length cDNA clones coding for cholineste
A;Reference number: A26613; MUID:87231856; PMID:3035536
A;Accession: A26613
A;Molecule type: mRNA
A;Residues: 1-133,'D',135-602 <PRO>
R;McTiernan, C.; Adkins, S.; Chatonnet, A.; Vaughan, T.A.; Bartels, C.F.; Kott, M.; Rose
Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987
A;Title: Brain cDNA clone for human cholinesterase.
A;Reference number: A33887; MUID:88016155; PMID:3477799
A;Accession: A33887
A;Molecule type: mRNA
A;Residues: 'MSVQSNLQAGAAAASCISPKYYMIFTPCKLYHLCCRESEIN',1-602 <MCT>
A;Note: two ATG codons found upstream of Met-1 do not lie in a favorable context for tra
R;Nogueira, C.P.; McGuire, M.C.; Graeser, C.; Bartels, C.F.; Arpagaus, M.; Van der Spek,
Am. J. Hum. Genet. 46, 934-942, 1990
A;Title: Identification of a frameshift mutation responsible for the silent phenotype of
A;Reference number: A34668; MUID:90252779; PMID:2339692
A;Accession: A34668
A;Molecule type: DNA
A;Residues: 143-145,'VSNWNIIFTCL' <NOG>
A;Note: frameshift mutant in codon for residue 145 (Gly)
R;Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S.E.; Johnson, L.L.
J. Biol. Chem. 262, 549-557, 1987
A;Title: Complete amino acid sequence of human serum cholinesterase.
A;Reference number: A00772; MUID:87109144; PMID:3542989
A;Accession: A00772
A;Molecule type: protein
A;Residues: 29-602 <LOC>
A;Experimental source: plasma
C;Comment: Cholinesterase is present in most cells (except erythrocytes).
C;Genetics:
A;Gene: GDB:BCHE; CHE1
A;Cross-references: GDB:120558; OMIM:177400
A;Map position: 3q26.1-3q26.2
A;Introns: 506/2; 562/1
C;Function:
A;Description: hydrolyzes acylcholines to choline and a carboxylic acid
A;Note: this cholinesterase is highly reactive with organophosphate esters
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-602/Product: cholinesterase #status experimental <MAT>
F;56-556/Domain: cholinesterase homology <CHE>
F;45,85,134,269,284,369,483,509,514/Binding site: carbohydrate (Asn) (covalent) #status
F;226/Active site: Ser #status experimental

  Query Match             71.3%;  Score 62;  DB 1;  Length 602;
  Best Local Similarity   64.3%;  Pred. No. 0.061;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        573 AGFHRWNNYMMDWK 586


RESULT 10
C39768
cholinesterase (EC 3.1.1.8) - rabbit
N;Alternate names: butyrylcholinesterase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1992 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S10255; C39768
R;Jbilo, O.; Chatonnet, A.
Nucleic Acids Res. 18, 3990, 1990
A;Title: Complete sequence of rabbit butyrylcholinesterase.
A;Reference number: S10255; MUID:90326526; PMID:2374720
A;Accession: S10255
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-581 <JBI>
A;Cross-references: UNIPROT:P21927; EMBL:X52090; NID:g1476; PIDN:CAA36308.1; PID:g137027
R;Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog
J. Biol. Chem. 266, 6966-6974, 1991
```

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A;Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
A;Reference number: A39768; MUID:91201348; PMID:2016308
A;Accession: C39768
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 75-215 <ARP>
A;Cross-references: GB:M62779; NID:g164788; PIDN:AAA31169.1; PID:g164789
C;Genetics:
A;Introns: 485/2; 541/1
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F;35-535/Domain: cholinesterase homology <CHE>

  Query Match             70.1%;  Score 61;  DB 2;  Length 581;
  Best Local Similarity   64.3%;  Pred. No. 0.084;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | ||||::||: ||
Db        552 AGFHRWNNYMMAWK 565


RESULT 11
S70849
cholinesterase (EC 3.1.1.8) - mouse
N;Alternate names: butyrylcholine esterase
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: S70849; S15680; A39768
R;Taylor, P.
submitted to the EMBL Data Library, August 1992
A;Reference number: S70849
A;Accession: S70849
A;Molecule type: nucleic acid
A;Residues: 1-603 <TAY>
A;Cross-references: UNIPROT:Q03311; EMBL:M99492; NID:g191579; PIDN:AAA37328.1; PID:g1915
R;Rachinsky, T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-327, 1990
A;Title: Molecular cloning of mouse acetylcholinesterase: tissue distribution of alterna
A;Reference number: JH0314; MUID:90380429; PMID:2400605
A;Accession: S15680
A;Status: nucleic acid sequence not shown
A;Molecule type: nucleic acid
A;Residues: 30-128,'P',130-603 <RAC>
A;Cross-references: EMBL:M99492
R;Arpagaus, M.; Chatonnet, A.; Masson, P.; Newton, M.; Vaughan, T.A.; Bartels, C.F.; Nog
J. Biol. Chem. 266, 6966-6974, 1991
A;Title: Use of the polymerase chain reaction for homology probing of butyrylcholinester
A;Reference number: A39768; MUID:91201348; PMID:2016308
A;Accession: A39768
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 97-128,'P',130-237 <ARP>
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein
F;57-557/Domain: cholinesterase homology <CHE>

  Query Match             70.1%;  Score 61;  DB 2;  Length 603;
  Best Local Similarity   64.3%;  Pred. No. 0.088;
  Matches    9;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | |||||:||: |:
Db        574 AGFHRWSNYMMDWQ 587


RESULT 12
T12393
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Arabidopsis thaliana chloroplast
C;Species: chloroplast Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12393
R;Galloway, G.L.; Malmberg, R.L.; Price, R.A.
Mol. Biol. Evol. 15, 1312-1320, 1998
A;Title: Phylogenetic utility of the nuclear gene arginine decarboxylase: an example fro
A;Reference number: Z16357; MUID:99003705; PMID:9787437
A;Accession: T12393
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-260 <GAL>
A;Cross-references: UNIPROT:O78318; EMBL:AF064654; NID:g3366917; PID:g3366918; PIDN:AAC6
C;Genetics:
A;Genome: chloroplast
A;Note: ndhF
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

  Query Match             50.6%;  Score 44;  DB 2;  Length 260;
  Best Local Similarity   41.7%;  Pred. No. 16;
  Matches    5;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 FHRWSSYMVHWK 14
              | :|:|  :||:
Db        192 FQKWNSKRIHWE 203


RESULT 13
D86339
protein F2D10.14 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86339
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86339
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-422 <STO>
A;Cross-references: UNIPROT:Q9LM89; GB:AE005172; NID:g8886950; PIDN:AAF80636.1; GSPDB:GN
C;Genetics:
A;Gene: F2D10.14
A;Map position: 1
C;Superfamily: Arabidopsis thaliana hypothetical protein At2g23160

  Query Match             49.4%;  Score 43;  DB 2;  Length 422;
  Best Local Similarity   50.0%;  Pred. No. 35;
  Matches    9;  Conservative    2;  Mismatches    3;  Indels    4;  Gaps    1;

Qy          1 AEFHRWSSYMV----HWK 14
              || |:||||:      ||
Db        328 AEKHQWSSYIYVLPPPWK 345


RESULT 14
S67037
SMP3 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O3527; protein YOR149c
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S67037; S13750
R;Bordonne, R.; Camasses, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarassov, I.A.; Winso
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67032
A;Accession: S67037
A;Molecule type: DNA
A;Residues: 1-516 <BOR>
A;Cross-references: UNIPROT:Q04174; EMBL:Z75057; NID:g1420374; PID:e252038; PID:g1420375
```

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A;Experimental source: strain S288C
R;Irie, K.; Araki, H.; Oshima, Y.
Mol. Gen. Genet. 225, 257-265, 1991
A;Title: Mutations in a Saccharomyces cerevisiae host showing increased holding stabilit
A;Reference number: S13750; MUID:91172125; PMID:2005867
A;Accession: S13750
A;Molecule type: DNA
A;Residues: 1-121,'IK',124-162,'G',164-168,'R',170-278,'L',280-516 <IRI>
A;Cross-references: EMBL:X58121; NID:g4497; PIDN:CAA41123.1; PID:g4498
C;Genetics:
A;Gene: SGD:SMP3
A;Cross-references: SGD:S0005675; MIPS:YOR149c
A;Map position: 15R
C;Keywords: transmembrane protein
F;9-25/Domain: transmembrane #status predicted <TM1>
F;189-205/Domain: transmembrane #status predicted <TM2>
F;215-231/Domain: transmembrane #status predicted <TM3>
F;271-287/Domain: transmembrane #status predicted <TM4>
F;344-360/Domain: transmembrane #status predicted <TM5>

  Query Match             49.4%;  Score 43;  DB 2;  Length 516;
  Best Local Similarity   66.7%;  Pred. No. 43;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 WSSYMVHWK 14
              |  | ||||
Db        204 WKFYRVHWK 212


RESULT 15
A87273
conserved hypothetical protein CC0194 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87273
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87273
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <STO>
A;Cross-references: UNIPROT:Q9ABN2; GB:AE005673; NID:g13421317; PIDN:AAK22181.1; GSPDB:G
C;Genetics:
A;Gene: CC0194

  Query Match             48.3%;  Score 42;  DB 2;  Length 100;
  Best Local Similarity   53.8%;  Pred. No. 13;
  Matches    7;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              |||| | :|  |:
Db         64 EFHRASPHMAAWR 76


RESULT 16
T08878
supervillin P205 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08878
R;Pestonjamasp, K.N.; Pope, R.K.; Wulfkuhle, J.D.; Luna, E.J.
J. Cell Biol. 139, 1255-1269, 1997
A;Title: Supervillin (P205): A novel membrane associated membrane associated F-actin bin
A;Reference number: Z16509; MUID:98044228; PMID:9382871
A;Accession: T08878
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1792 <PES>
A;Cross-references: UNIPROT:O46385; EMBL:AF025996; NID:g2668622; PIDN:AAC48783.1; PID:g2
A;Experimental source: cell line MDBK (Madin Darby Bovine Kidney); ATCC CCL-22
C;Keywords: actin binding; cell adhesion; membrane-associated protein
F;1732-1792/Domain: villin headpiece homology <VHH>

  Query Match             48.3%;  Score 42;  DB 2;  Length 1792;
  Best Local Similarity   46.2%;  Pred. No. 2e+02;
  Matches    6;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHWK 14
              :||   :|:| ||
Db       1352 QFHEGDAYVVKWK 1364


RESULT 17
C96911
transcription regulators, LysR family [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: C96911
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo.
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C96911
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-290 <KUR>
A;Cross-references: UNIPROT:Q97MU8; GB:AE001437; PIDN:AAK78078.1; PID:g15022917; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0093

  Query Match             47.1%;  Score 41;  DB 2;  Length 290;
  Best Local Similarity   54.5%;  Pred. No. 50;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVH 12
              |:||: ||: |
Db        262 EYHRYFSYLCH 272


RESULT 18
A75137
hypothetical protein PAB0600 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A75137
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: A75137
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <KAW>
A;Cross-references: UNIPROT:Q9V095; GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB4981
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB0600

  Query Match             47.1%;  Score 41;  DB 2;  Length 397;
  Best Local Similarity   40.0%;  Pred. No. 68;
  Matches    6;  Conservative    3;  Mismatches    4;  Indels    2;  Gaps    1;

Qy          2 EFH--RWSSYMVHWK 14
              ::|  ||    :|||
Db         18 DYHVKRWKEQKLHWK 32


RESULT 19
F96741
probable sucrose transport protein F17M19.4 [imported] - Arabidopsis thaliana
```

```
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F96741
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F96741
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-512 <STO>
A;Cross-references: UNIPROT:Q9C8X2; GB:AE005173; NID:g6978914; PIDN:AAF34306.1; GSPDB:GN
C;Genetics:
A;Gene: F17M19.4
A;Map position: 1
C;Superfamily: common tobacco sucrose transport protein

  Query Match             47.1%;  Score 41;  DB 2;  Length 512;
  Best Local Similarity   85.7%;  Pred. No. 86;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HRWSSYM 10
              |:|||||
Db         66 HKWSSYM 72


RESULT 20
A97177
site-specific recombinase, DNA invertase Pin homolog [imported] - Clostridium acetobutyl
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97177
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A97177
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-523 <KUR>
A;Cross-references: UNIPROT:Q97GW8; GB:AE001437; PIDN:AAK80204.1; PID:g15025248; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC2247

  Query Match             47.1%;  Score 41;  DB 2;  Length 523;
  Best Local Similarity   55.6%;  Pred. No. 88;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 HRWSSYMVH 12
              ||| :||::
Db        231 HRWQAYMIN 239


RESULT 21
B83936
hypothetical protein BH2290 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: B83936
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83936
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-535 <STO>
A;Cross-references: UNIPROT:Q9KAJ7; GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB060
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2290

  Query Match             47.1%;  Score 41;  DB 2;  Length 535;
  Best Local Similarity   70.0%;  Pred. No. 90;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMV 11
              :|||| | ||
Db        172 KFHRWFSLMV 181


RESULT 22
H83904
hypothetical protein BH2040 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H83904
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H83904
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-818 <STO>
A;Cross-references: UNIPROT:Q9KB88; GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB057
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2040

  Query Match             47.1%;  Score 41;  DB 2;  Length 818;
  Best Local Similarity   45.5%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 HRWSSYMVHWK 14
              : |||::: ||
Db        369 NEWSSHLITWK 379


RESULT 23
T30253
spalt protein - mouse (fragment)
N;Alternate names: zinc finger protein msa1
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30253
R;Ott, T.; Kaestner, K.H.; Monaghan, A.P.; Schutz, G.
Mech. Dev. 56, 117-128, 1996
A;Title: The mouse homolog of the region specific homeotic gene spalt of Drosophila is e
A;Reference number: Z20791; MUID:96391179; PMID:8798152
A;Accession: T30253
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1323 <OTT>
A;Cross-references: UNIPROT:Q62255; EMBL:X97581; NID:g1296844; PIDN:CAA66196.1; PID:g129
C;Genetics:
A;Gene: msa1
C;Function:
A;Description: may play an important role in the development of the nervous system

  Query Match             47.1%;  Score 41;  DB 2;  Length 1323;
  Best Local Similarity   42.9%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||| :|: :: | |
Db         29 AEFFKWADFLQHKK 42
```

```
RESULT 24
S64059
stearoyl-CoA 9-desaturase (EC 1.14.19.1) - yeast (Saccharomyces cerevisiae)
N;Alternate names: Delta9 fatty acid desaturase; protein G3472; protein YGL055w
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: S64059; A23675
R;Feuermann, M.; Potier, S.; Souciet, J.L.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64044
A;Accession: S64059
A;Molecule type: DNA
A;Residues: 1-510 <FEU>
A;Cross-references: UNIPROT:P21147; EMBL:Z72577; NID:g1322551; PIDN:CAA96757.1; PID:g132
A;Experimental source: strain S288C
R;Stukey, J.E.; McDonough, V.M.; Martin, C.E.
J. Biol. Chem. 265, 20144-20149, 1990
A;Title: The OLE1 gene of Saccharomyces cerevisiae encodes the delta9 fatty acid desatur
A;Reference number: A23675; MUID:91056050; PMID:1978720
A;Accession: A23675
A;Molecule type: DNA
A;Residues: 1-303,'M',305-510 <STU>
A;Cross-references: GB:J05676; NID:g172063; PIDN:AAA34826.1; PID:g172064
C;Genetics:
A;Gene: SGD:OLE1; MDM2; MIPS:YGL055w
A;Cross-references: SGD:S0003023; MIPS:YGL055w
A;Map position: 7L
C;Superfamily: Delta-9 acyl-CoA desaturase with heme/steroid binding domain; cytochrome
C;Keywords: endoplasmic reticulum; heme; iron; metalloprotein; oxidoreductase; transmemb
F;116-132/Domain: transmembrane #status predicted <TM1>
F;141-157/Domain: transmembrane #status predicted <TM2>
F;155-345/Domain: stearoyl-CoA desaturase homology <SDH>
F;257-273/Domain: transmembrane #status predicted <TM3>
F;409-486/Domain: cytochrome b5 core homology <CB5>
F;444,470/Binding site: heme iron (His) (axial ligands) #status predicted

  Query Match             46.6%;  Score 40.5;  DB 1;  Length 510;
  Best Local Similarity   56.2%;  Pred. No. 1e+02;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    3;  Gaps    2;

Qy          1 AEFHR-WS--SYMVHW 13
              | :|| ||  ||  ||
Db        158 AGYHRLWSHRSYSAHW 173


RESULT 25
PH1152
Ig heavy chain V region (clone 47F.2A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PH1152
R;Schittek, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A;Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A;Reference number: PH1105; MUID:92364545; PMID:1500855
A;Accession: PH1152
A;Molecule type: DNA
A;Residues: 1-90 <SCH>
A;Cross-references: UNIPROT:Q91VA2; UNIPROT:Q924Q4; UNIPROT:Q924Q6; UNIPROT:Q924Q9; UNIP
PROT:Q924P7; UNIPROT:Q924R1; UNIPROT:Q924R4; UNIPROT:Q924R0; UNIPROT:Q924Q8; UNIPROT:Q92
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

  Query Match             46.0%;  Score 40;  DB 2;  Length 90;
  Best Local Similarity   46.2%;  Pred. No. 23;
  Matches    6;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHW 13
              |  | ::|| :||
Db         16 ASGHTFTSYWMHW 28


RESULT 26
JC2104
hypothetical 20.8K protein - Zymomonas mobilis
C;Species: Zymomonas mobilis
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: JC2104
R;Kondo, Y.; Toyoda, A.; Fukushi, H.; Yanase, H.; Tonomura, K.; Kawasaki, H.; Sakai, T.
Biosci. Biotechnol. Biochem. 58, 526-530, 1994
A;Title: Cloning and characterization of a pair of genes that stimulate the production a
A;Reference number: JC2103; MUID:94227334; PMID:7764692
A;Accession: JC2104
A;Molecule type: DNA
A;Residues: 1-184 <KON>
A;Cross-references: UNIPROT:Q57000; GB:D17522; NID:g402545; PIDN:BAA04473.1; PID:g433223
A;Experimental source: strain Z6C
C;Comment: This protein stimulates the secretion of the extracellular levansucrase and i
C;Genetics:
A;Gene: zliS
C;Superfamily: Zymomonas mobilis hypothetical 20.8K protein

  Query Match             46.0%;  Score 40;  DB 2;  Length 184;
  Best Local Similarity   50.0%;  Pred. No. 46;
  Matches    7;  Conservative    3;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 AEFHRWSSYMVHWK 14
              |:| ||  |: ||:
Db          5 ADFIRW--YIQHWE 16


RESULT 27
B84035
hypothetical protein BH3082 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: B84035
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B84035
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-211 <STO>
A;Cross-references: UNIPROT:Q9K8C4; GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BAB068
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3082

  Query Match             46.0%;  Score 40;  DB 2;  Length 211;
  Best Local Similarity   50.0%;  Pred. No. 53;
  Matches    7;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              |:::|||   || |
Db        160 ADYNRWSRPAVHGK 173


RESULT 28
S64351
hypothetical protein YGR057c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G4346
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S64351
R;Entian, K.D.; Rose, M.; Koetter, P.; Roehmer, A.; Sehrsam, I.; Hempel, S.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64335
A;Accession: S64351
A;Molecule type: DNA
A;Residues: 1-245 <ENT>
```

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A;Cross-references: UNIPROT:P53237; EMBL:Z72842; NID:g1323070; PID:g1323071; GSPDB:GN000
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:LST7; MIPS:YGR057c
A;Cross-references: SGD:S0003289
A;Map position: 7R
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YGR057c

  Query Match             46.0%;  Score 40;  DB 2;  Length 245;
  Best Local Similarity   44.4%;  Pred. No. 61;
  Matches    4;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 HRWSSYMVH 12
              |:|:|:::|
Db        228 HKWNSFLLH 236


RESULT 29
A64546
hypothetical protein HP0209 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: A64546
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: A64546
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-450 <TOM>
A;Cross-references: UNIPROT:O25000; GB:AE000541; GB:AE000511; NID:g2313299; PIDN:AAD0728
C;Genetics:
A;Start codon: GTG
C;Superfamily: Helicobacter pylori hypothetical protein HP0209

  Query Match             46.0%;  Score 40;  DB 2;  Length 450;
  Best Local Similarity   36.4%;  Pred. No. 1.1e+02;
  Matches    4;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 FHRWSSYMVHW 13
              |:||  : : |
Db        179 FYRWKKFRIEW 189


RESULT 30
T30341
zinc finger protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30341
R;Hollemann, T.; Schuh, R.; Pieler, T.; Stick, R.
Mech. Dev. 55, 19-32, 1996
A;Title: Xenopus Xsal-1, a vertebrate homolog of the region specific homeotic gene spalt
A;Reference number: Z20832; MUID:96317243; PMID:8734496
A;Accession: T30341
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1350 <HOL>
A;Cross-references: UNIPROT:Q91929; EMBL:L46583; NID:g1235930; PID:g1235931; PIDN:AAC422
C;Genetics:
A;Note: Xsal-1

  Query Match             46.0%;  Score 40;  DB 2;  Length 1350;
  Best Local Similarity   42.9%;  Pred. No. 3.1e+02;
  Matches    6;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||| :|: :: | |
Db         70 AEFFKWTDFLDHKK 83


RESULT 31
T08166
probable membrane protein 1995 - Chlamydomonas reinhardtii chloroplast
C;Species: chloroplast Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C;Accession: T08166; A24829
R;Boudreau, E.; Turmel, M.; Goldschmidt-Clermont, M.; Rochaix, J.D.; Sivan, S.; Michaels
Mol. Gen. Genet. 253, 649-653, 1997
A;Title: A large unidentified open reading frame (ORF1995) in Chlamydomonas reinhardtii
A;Reference number: Z16392; MUID:97218038; PMID:9065699
A;Accession: T08166
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1995 <BOU>
A;Cross-references: UNIPROT:P36495; EMBL:X92726; NID:g1054719; PIDN:CAA63385.1; PID:g105
R;Woessner, J.P.; Gillham, N.W.; Boynton, J.E.
Gene 44, 17-28, 1986
A;Title: The sequence of the chloroplast atpB gene and its flanking regions in Chlamydom
A;Reference number: A24829; MUID:87031585; PMID:2876928
A;Accession: A24829
A;Molecule type: DNA
A;Residues: 1925-1995 <WOE>
A;Cross-references: GB:M13704; NID:g336666; PIDN:AAA84144.1; PID:g895614
A;Note: the authors translated the codon GAA for residue 1957 as Gly
C;Genetics:
A;Genome: chloroplast
C;Keywords: chloroplast; membrane protein

  Query Match             46.0%;  Score 40;  DB 2;  Length 1995;
  Best Local Similarity   60.0%;  Pred. No. 4.5e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 RWSSYMVHWK 14
              || :|| |:|
Db        882 RWYTYMQHYK 891


RESULT 32
S74825
probable Rieske iron-sulfur protein slr1747 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74825
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74825
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-469 <KAN>
A;Cross-references: UNIPROT:P73738; EMBL:D90909; GB:AB001339; NID:g1652844; PIDN:BAA1778
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Nostoc sp. cell death suppressor protein; Rieske [2Fe-2S] homology
C;Keywords: 2Fe-2S; metalloprotein; Rieske iron-sulfur protein
F;66-114/Domain: Rieske [2Fe-2S] homology <RSK>
F;76,78,96,99/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status predi

  Query Match             45.4%;  Score 39.5;  DB 2;  Length 469;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 AEFHRW-SSYMV 11
              ||||||   | |
Db        349 AEFHRWIEQYQV 360


RESULT 33
```

```
T02379
hypothetical protein At2g44230 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F4I1.4
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02379; A84876
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence.
A;Reference number: Z14667
A;Accession: T02379
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-542 <ROU>
A;Cross-references: UNIPROT:O64858; EMBL:AC004521; NID:g3128166; PID:g3128170
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84876
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-542 <STO>
A;Cross-references: GB:AE002093; NID:g3128170; PIDN:AAC16074.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g44230; F4I1.4
A;Map position: 2
A;Introns: 32/1

  Query Match             45.4%;  Score 39.5;  DB 2;  Length 542;
  Best Local Similarity   40.0%;  Pred. No. 1.5e+02;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    7;  Gaps    1;

Qy          1 AEFHR-------WSSYMVHW 13
              ||: |       | :|| ||
Db        464 AEYMRGELEEPAWLNYMRHW 483


RESULT 34
T09856
sucrose synthase (EC 2.4.1.13) - upland cotton (fragment)
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09856
R;Shimizu, Y.; Aotsuka, S.; Hasegawa, O.; Kawada, T.; Sakuno, T.; Sakai, F.; Hayashi, T.
Plant Cell Physiol. 38, 375-378, 1997
A;Title: Changes in levels of mRNAs for cell wall-related enzymes in growing cotton fibe
A;Reference number: Z16889; MUID:97294938; PMID:9150611
A;Accession: T09856
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-100 <SHI>
A;Cross-references: UNIPROT:O23949; EMBL:D88412; NID:g2244729; PIDN:BAA21106.1; PID:g224
A;Experimental source: strain Coker312; fiber
C;Function:
A;Description: catalyzes reversible cleavage of sucrose into UDP-glucose and D-fructose
C;Superfamily: sucrose synthase; sucrose/sucrose-phosphate synthase homology
C;Keywords: glycosyltransferase; hexosyltransferase

  Query Match             44.8%;  Score 39;  DB 2;  Length 100;
  Best Local Similarity   35.7%;  Pred. No. 37;
  Matches    5;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              | | | : :::||:
Db         80 ASFPRXNRFLIHWQ 93


RESULT 35
HVMST7
Ig heavy chain precursor V region (TEPC 1017) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C;Accession: A02033
R;Gilliam, A.C.; Shen, A.; Richards, J.E.; Blattner, F.R.; Mushinski, J.F.; Tucker, P.W.
Proc. Natl. Acad. Sci. U.S.A. 81, 4164-4168, 1984
A;Title: Illegitimate recombination generates a class switch from C-mu to C-delta in an
A;Reference number: A02033; MUID:84248078; PMID:6429663
A;Accession: A02033
A;Molecule type: mRNA
A;Residues: 1-138 <GIL>
A;Cross-references: UNIPROT:P03980
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-138/Product: Ig heavy chain V region (TEPC 1017) #status predicted <MAT>
F;21-117/Region: V segment
F;34-117/Domain: immunoglobulin homology <IMM>
F;118-123/Region: D segment
F;124-138/Region: J segment

  Query Match             44.8%;  Score 39;  DB 1;  Length 138;
  Best Local Similarity   38.5%;  Pred. No. 50;
  Matches    5;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHW 13
              |  | :::| :||
Db         43 ASGHTFTNYWIHW 55


RESULT 36
B82315
hypothetical protein VC0496 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82315
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82315
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <HEI>
A;Cross-references: UNIPROT:Q9KUL9; GB:AE004136; GB:AE003852; NID:g9654921; PIDN:AAF9366
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0496
A;Map position: 1
C;Superfamily: yagK protein

  Query Match             44.8%;  Score 39;  DB 2;  Length 199;
  Best Local Similarity   58.3%;  Pred. No. 71;
  Matches    7;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 FHRWSSYMVHWK 14
              ||| ||:   ||
Db        177 FHRLSSFAEAWK 188


RESULT 37
S37434
membrane glycoprotein - porcine epidemic diarrhea virus
C;Species: porcine epidemic diarrhea virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S37434
R;Duarte, M.
submitted to the EMBL Data Library, July 1993
A;Reference number: S37432
A;Accession: S37434
A;Status: preliminary
```

```
A;Molecule type: genomic RNA
A;Residues: 1-226 <DUA>
A;Cross-references: UNIPROT:P59771; UNIPROT:P59770; EMBL:Z24733; NID:g406754; PIDN:CAA80
C;Superfamily: coronavirus E1 membrane glycoprotein

  Query Match             44.8%;  Score 39;  DB 2;  Length 226;
  Best Local Similarity   45.5%;  Pred. No. 80;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 FHRWSSYMVHW 13
              |  |:|: |:|
Db         65 FDAWASFQVNW 75


RESULT 38
D49591
membrane protein M - porcine epidemic diarrhea virus
C;Species: porcine epidemic diarrhea virus
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: D49591
R;Duarte, M.; Tobler, K.; Bridgen, A.; Rasschaert, D.; Ackermann, M.; Laude, H.
Virology 198, 466-476, 1994
A;Title: Sequence analysis of the porcine epidemic diarrhea virus genome between the nuc
A;Reference number: A49591; MUID:94120721; PMID:8291230
A;Accession: D49591
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-226 <DUA>
A;Cross-references: UNIPROT:Q91AU9; GB:Z24733
C;Superfamily: coronavirus E1 membrane glycoprotein

  Query Match             44.8%;  Score 39;  DB 2;  Length 226;
  Best Local Similarity   45.5%;  Pred. No. 80;
  Matches    5;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 FHRWSSYMVHW 13
              |  |:|: |:|
Db         65 FDAWASFQVNW 75


RESULT 39
T12386
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Sisymbrium altissimum chloroplas
C;Species: chloroplast Sisymbrium altissimum
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12386
R;Galloway, G.L.; Malmberg, R.L.; Price, R.A.
Mol. Biol. Evol. 15, 1312-1320, 1998
A;Title: Phylogenetic utility of the nuclear gene arginine decarboxylase: an example frc
A;Reference number: Z16357; MUID:99003705; PMID:9787437
A;Accession: T12386
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-259 <GAL>
A;Cross-references: UNIPROT:O78312; EMBL:AF064648; NID:g3366905; PID:g3366906; PIDN:AAC6
C;Genetics:
A;Genome: chloroplast
A;Note: ndhF
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

  Query Match             44.8%;  Score 39;  DB 2;  Length 259;
  Best Local Similarity   41.7%;  Pred. No. 91;
  Matches    5;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 FHRWSSYMVHWK 14
              | :|||  : |:
Db        192 FQKWSSKRIRWE 203


RESULT 40
T12395
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Thlaspi arvense chloroplast (fra
C;Species: chloroplast Thlaspi arvense
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12395
R;Galloway, G.L.; Malmberg, R.L.; Price, R.A.
Mol. Biol. Evol. 15, 1312-1320, 1998
A;Title: Phylogenetic utility of the nuclear gene arginine decarboxylase: an example fro
A;Reference number: Z16357; MUID:99003705; PMID:9787437
A;Accession: T12395
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-260 <GAL>
A;Cross-references: UNIPROT:O78320; EMBL:AF064656; NID:g3366921; PID:g3366922; PIDN:AAC6
C;Genetics:
A;Genome: chloroplast
A;Note: ndhF
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

  Query Match             44.8%;  Score 39;  DB 2;  Length 260;
  Best Local Similarity   41.7%;  Pred. No. 91;
  Matches    5;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 FHRWSSYMVHWK 14
              | :|||  : |:
Db        192 FQKWSSKRIRWE 203


RESULT 41
T12394
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Stanleya pinnata chloroplast (fr
C;Species: chloroplast Stanleya pinnata
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12394
R;Galloway, G.L.; Malmberg, R.L.; Price, R.A.
Mol. Biol. Evol. 15, 1312-1320, 1998
A;Title: Phylogenetic utility of the nuclear gene arginine decarboxylase: an example frc
A;Reference number: Z16357; MUID:99003705; PMID:9787437
A;Accession: T12394
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-260 <GAL>
A;Cross-references: UNIPROT:O78319; EMBL:AF064655; NID:g3366919; PID:g3366920; PIDN:AAC6
C;Genetics:
A;Genome: chloroplast
A;Note: ndhF
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

  Query Match             44.8%;  Score 39;  DB 2;  Length 260;
  Best Local Similarity   41.7%;  Pred. No. 91;
  Matches    5;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 FHRWSSYMVHWK 14
              | :|||  : |:
Db        192 FQKWSSKRIRWE 203


RESULT 42
T14435
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - wild cabbage chloroplast (fragme
C;Species: chloroplast Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14435
R;Galloway, G.L.; Malmberg, R.L.; Price, R.A.
Mol. Biol. Evol. 15, 1312-1320, 1998
A;Title: Phylogenetic utility of the nuclear gene arginine decarboxylase: an example frc
A;Reference number: Z16357; MUID:99003705; PMID:9787437
A;Accession: T14435
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-260 <GAL>
A;Cross-references: UNIPROT:O78311; EMBL:AF064647; NID:g3366903; PIDN:AAC68586.1; PID:g3
C;Genetics:
```

```
A;Gene: ndhF
A;Genome: chloroplast
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

  Query Match            44.8%;  Score 39;  DB 2;  Length 260;
  Best Local Similarity  41.7%;  Pred. No. 91;
  Matches    5;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 FHRWSSYMVHWK 14
              | :|||  : |:
Db        192 FQKWSSKRIRWE 203


RESULT 43
F89904
glycerol uptake facilitator [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F89904
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: F89904
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-272 <KUR>
A;Cross-references: UNIPROT:Q99UH4; GB:BA000018; PID:g13701099; PIDN:BAB42394.1; GSPDB:G
A;Experimental source: strain N315
C;Genetics:
A;Gene: glpF

  Query Match            44.8%;  Score 39;  DB 2;  Length 272;
  Best Local Similarity  55.6%;  Pred. No. 95;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 WSSYMVHWK 14
              |  |: |||
Db        101 WLMYLPHWK 109


RESULT 44
D83191
conserved hypothetical protein PA3631 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83191
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83191
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-408 <STO>
A;Cross-references: UNIPROT:Q9HXZ9; GB:AE004783; GB:AE004091; NID:g9949786; PIDN:AAG0701
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3631
C;Superfamily: Campylobacter jejuni probable integral membrane protein Cj1500

  Query Match            44.8%;  Score 39;  DB 2;  Length 408;
  Best Local Similarity  41.7%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 EFHRWSSYMVHW 13
              || ||  ::: |
Db         45 EFTRWGGHVLSW 56


RESULT 45
B42249
serine-type carboxypeptidase (EC 3.4.16.-) sxa2 - fission yeast (Schizosaccharomyces pom
C;Species: Schizosaccharomyces pombe
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 16-Aug-2004
C;Accession: B42249; T37564
R;Imai, Y.; Yamamoto, M.
Mol. Cell. Biol. 12, 1827-1834, 1992
A;Title: Schizosaccharomyces pombe sxa1(+) and sxa2(+) encode putative proteases involve
A;Reference number: A42249; MUID:92195329; PMID:1549128
A;Accession: B42249
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-507 <IMA>
A;Cross-references: UNIPROT:P32825; GB:D10199; NID:g218559; PIDN:BAA01047.1; PID:g218560
R;Wood, V.; Barrell, B.G.; Rajandream, M.A.; Harris, D.; Seeger, K.
submitted to the EMBL Data Library, February 1999
A;Reference number: Z21725
A;Accession: T37564
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-507 <WOO>
A;Cross-references: EMBL:AL035439; PIDN:CAB36509.1; GSPDB:GN00066; SPDB:SPAC1296.03c
A;Experimental source: strain 972h-; cosmid c1296
C;Genetics:
A;Gene: sxa2
A;Map position: 1
C;Superfamily: Serine carboxypeptidase
C;Keywords: hydrolase; serine carboxypeptidase

  Query Match            44.8%;  Score 39;  DB 2;  Length 507;
  Best Local Similarity  54.5%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 HRWSSYMVHWK 14
              |   :| ||||
Db         21 HALPTYTVHWK 31


Search completed: October 12, 2005, 10:20:09
Job time : 27 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 12, 2005, 10:06:29 ; Search time 165 Seconds
(without alignments)
32.816 Million cell updates/sec

Title: US-09-155-076-1
Perfect score: 87
Sequence: 1 AEFHRWSSYMVHWK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	87	100.0	14	2	AAW35340	Aaw35340 Human ace
2	87	100.0	14	4	AAU04701	Aau04701 Scrambled
3	87	100.0	14	5	ABG65979	Abg65979 Human ace
4	87	100.0	39	2	AAR77010	Aar77010 Alternati
5	87	100.0	40	4	AAB48915	Aab48915 Human ace
6	87	100.0	40	4	AAB50033	Aab50033 Acetylcho
7	87	100.0	40	5	AAU98023	Aau98023 Human syn
8	87	100.0	44	4	AAU04705	Aau04705 Rat acety
9	87	100.0	44	4	AAU04704	Aau04704 Mouse ace
10	87	100.0	44	4	AAU04702	Aau04702 Human ace
11	87	100.0	44	4	AAG65951	Aag65951 Mouse ace
12	87	100.0	44	4	AAG65949	Aag65949 Human ace
13	87	100.0	44	4	AAG65952	Aag65952 Rat acety
14	87	100.0	45	2	AAW74586	Aaw74586 Amino aci
15	87	100.0	45	2	AAW48800	Aaw48800 C-termina
16	87	100.0	45	2	AAW68144	Aaw68144 Human ACh
17	87	100.0	53	4	AAU04299	Aau04299 Bovine ac
18	87	100.0	53	4	AAG65953	Aag65953 Bovine ac
19	87	100.0	54	4	AAU04703	Aau04703 Rabbit ac
20	87	100.0	54	4	AAG65950	Aag65950 Rabbit ac
21	87	100.0	67	4	AAB50037	Aab50037 Acetylcho
22	87	100.0	68	5	ABG31332	Abg31332 GFP-fused
23	87	100.0	348	8	ADL90218	Adl90218 Human enz
24	87	100.0	469	8	ABM83175	Abm83175 Human dia
25	87	100.0	500	2	AAR06990	Aar06990 Human foe
26	87	100.0	526	6	ABR38991	Abr38991 Human ace
27	87	100.0	526	8	ADR21588	Adr21588 Human enz
28	87	100.0	583	3	AAG80773	Aag80773 AchE prot
29	87	100.0	584	3	AAG80772	Aag80772 AchE prot
30	87	100.0	613	2	AAR06989	Aar06989 Human ace
31	87	100.0	614	2	AAR80726	Aar80726 Human ace
32	87	100.0	614	3	AAY49490	Aay49490 Human ace
33	87	100.0	614	3	AAY49489	Aay49489 Human wil
34	87	100.0	614	3	AAY49493	Aay49493 Human ace
35	87	100.0	614	3	AAY49492	Aay49492 Human ace
36	87	100.0	614	3	AAY49491	Aay49491 Human ace
37	87	100.0	614	3	AAY49495	Aay49495 Human ace
38	87	100.0	614	3	AAY49494	Aay49494 Human ace
39	87	100.0	614	5	AAU11231	Aau11231 Human ace
40	87	100.0	614	5	AAU11232	Aau11232 Human ace
41	87	100.0	614	5	AAU11234	Aau11234 Human ace
42	87	100.0	614	5	AAU11233	Aau11233 Human ace
43	87	100.0	614	6	ABP59222	Abp59222 Human dru
44	87	100.0	614	6	ABB99726	Abb99726 Amino aci
45	87	100.0	614	7	ADE61695	Ade61695 Rat Prote
46	87	100.0	614	7	ADE61697	Ade61697 Human Pro
47	87	100.0	614	7	ADE61689	Ade61689 Human Pro
48	87	100.0	614	7	ADE61687	Ade61687 Rat Prote
49	87	100.0	614	7	ADE61683	Ade61683 Rat Prote
50	87	100.0	614	7	ADE61691	Ade61691 Rat Prote
51	87	100.0	614	7	ADE61693	Ade61693 Human Pro
52	87	100.0	614	7	ADE61685	Ade61685 Human Pro
53	87	100.0	614	8	ADQ89842	Adq89842 Antagonis
54	87	100.0	620	5	AAU11235	Aau11235 Human ace
55	84	96.6	14	5	ABG66007	Abg66007 Human ace
56	84	96.6	14	5	ABG66017	Abg66017 Human ace
57	84	96.6	14	5	ABG65988	Abg65988 Human ace
58	84	96.6	14	5	ABG66018	Abg66018 Human ace
59	84	96.6	14	5	ABG65989	Abg65989 Human ace
60	83	95.4	13	5	ABG66025	Abg66025 Human ace
61	83	95.4	14	5	ABG65983	Abg65983 Human ace
62	83	95.4	14	5	ABG65986	Abg65986 Human ace
63	83	95.4	14	5	ABG66021	Abg66021 Human ace
64	83	95.4	14	5	ABG66002	Abg66002 Human ace
65	82	94.3	13	5	ABG66035	Abg66035 Human ace
66	82	94.3	14	5	ABG66004	Abg66004 Human ace
67	82	94.3	14	5	ABG65981	Abg65981 Human ace
68	82	94.3	14	5	ABG66045	Abg66045 Human ace
69	82	94.3	14	5	ABG66024	Abg66024 Human ace
70	81	93.1	14	5	ABG66020	Abg66020 Human ace
71	81	93.1	14	5	ABG66015	Abg66015 Human ace
72	81	93.1	14	5	ABG66012	Abg66012 Human ace
73	80	92.0	14	5	ABG66005	Abg66005 Human ace
74	80	92.0	14	5	ABG66008	Abg66008 Human ace
75	80	92.0	14	5	ABG65984	Abg65984 Human ace
76	80	92.0	14	5	ABG65987	Abg65987 Human ace
77	80	92.0	14	5	ABG65990	Abg65990 Human ace
78	80	92.0	575	2	AAW39079	Aaw39079 Torpedo c
79	80	92.0	575	2	AAW39078	Aaw39078 Torpedo c
80	80	92.0	576	7	ABR84598	Abr84598 T califon
81	80	92.0	576	8	ADM42074	Adm42074 Torpedo c
82	80	92.0	576	8	ADM42073	Adm42073 Torpedo c
83	79	90.8	14	5	ABG66013	Abg66013 Human ace
84	79	90.8	14	5	ABG65980	Abg65980 Human ace
85	79	90.8	14	5	ABG66003	Abg66003 Human ace
86	78	89.7	12	5	ABG66046	Abg66046 Human ace
87	78	89.7	12	5	ABG66026	Abg66026 Human ace
88	78	89.7	14	5	ABG65991	Abg65991 Human ace
89	78	89.7	14	5	ABG66019	Abg66019 Human ace
90	78	89.7	27	4	AAB48916	Aab48916 Human ace
91	78	89.7	27	4	AAB50034	Aab50034 Acetylcho
92	77	88.5	14	5	ABG66011	Abg66011 Human ace
93	77	88.5	14	5	ABG66014	Abg66014 Human ace
94	77	88.5	14	5	ABG66022	Abg66022 Human ace
95	77	88.5	14	5	ABG66009	Abg66009 Human ace
96	77	88.5	14	5	ABG65998	Abg65998 Human ace
97	75	86.2	14	5	ABG66010	Abg66010 Human ace
98	75	86.2	14	5	ABG66006	Abg66006 Human ace

99	74	85.1	14	5	ABG65985	Abg65985 Human ace
100	74	85.1	14	5	ABG65992	Abg65992 Human ace
101	74	85.1	14	5	ABG65999	Abg65999 Human ace
102	73	83.9	14	5	ABG66023	Abg66023 Human ace
103	73	83.9	14	5	ABG66016	Abg66016 Human ace
104	72	82.8	11	5	ABG66027	Abg66027 Human ace
105	72	82.8	14	5	ABG65982	Abg65982 Human ace
106	71	81.6	12	5	ABG66036	Abg66036 Human ace
107	67	77.0	14	5	ABG66000	Abg66000 Human ace
108	65	74.7	574	5	AAO18903	Aao18903 Horse but
109	65	74.7	574	8	ADR01083	Adr01083 Rat butyr
110	64	73.6	10	5	ABG66028	Abg66028 Human ace
111	63	72.4	11	5	ABG66037	Abg66037 Human ace
112	62	71.3	10	5	ABG66047	Abg66047 Human ace
113	62	71.3	574	5	AAE25235	Aae25235 Human but
114	62	71.3	574	5	AAO18934	Aao18934 Human but
115	62	71.3	574	5	AAO18977	Aao18977 Human but
116	62	71.3	574	5	AAO18957	Aao18957 Human but
117	62	71.3	574	5	AAO18968	Aao18968 Human but
118	62	71.3	574	5	AAO18899	Aao18899 Human but
119	62	71.3	574	5	AAO18900	Aao18900 Human but
120	62	71.3	574	5	AAO18949	Aao18949 Human but
121	62	71.3	574	5	AAO18956	Aao18956 Human but
122	62	71.3	574	5	AAO18926	Aao18926 Human but
123	62	71.3	574	5	AAO18939	Aao18939 Human but
124	62	71.3	574	5	AAO18943	Aao18943 Human but
125	62	71.3	574	5	AAO18963	Aao18963 Human but
126	62	71.3	574	5	AAO18981	Aao18981 Human but
127	62	71.3	574	5	AAO18901	Aao18901 Human but
128	62	71.3	574	5	AAO18927	Aao18927 Human but
129	62	71.3	574	5	AAO18932	Aao18932 Human but
130	62	71.3	574	5	AAO18940	Aao18940 Human but
131	62	71.3	574	5	AAO18942	Aao18942 Human but
132	62	71.3	574	5	AAO18950	Aao18950 Human but
133	62	71.3	574	5	AAO18951	Aao18951 Human but
134	62	71.3	574	5	AAO18959	Aao18959 Human but
135	62	71.3	574	5	AAO18960	Aao18960 Human but
136	62	71.3	574	5	AAO18975	Aao18975 Human but
137	62	71.3	574	5	AAO18982	Aao18982 Human but
138	62	71.3	574	5	AAO18952	Aao18952 Human but
139	62	71.3	574	5	AAO18972	Aao18972 Human but
140	62	71.3	574	5	AAO18974	Aao18974 Human but
141	62	71.3	574	5	AAO18953	Aao18953 Human but
142	62	71.3	574	5	AAO18958	Aao18958 Human but
143	62	71.3	574	5	AAO18970	Aao18970 Human but
144	62	71.3	574	5	AAO18971	Aao18971 Human but
145	62	71.3	574	5	AAO18930	Aao18930 Human but
146	62	71.3	574	5	AAO18944	Aao18944 Human but
147	62	71.3	574	5	AAO18978	Aao18978 Human but
148	62	71.3	574	5	AAO18983	Aao18983 Human but
149	62	71.3	574	5	AAO18929	Aao18929 Human but
150	62	71.3	574	5	AAO18933	Aao18933 Human but
151	62	71.3	574	5	AAO18938	Aao18938 Human but
152	62	71.3	574	5	AAO18979	Aao18979 Human but
153	62	71.3	574	5	AAO18980	Aao18980 Human but
154	62	71.3	574	5	AAO18905	Aao18905 Rat butyr
155	62	71.3	574	5	AAO18945	Aao18945 Human but
156	62	71.3	574	5	AAO18967	Aao18967 Human but
157	62	71.3	574	5	AAO18902	Aao18902 Human but
158	62	71.3	574	5	AAO18935	Aao18935 Human but
159	62	71.3	574	5	AAO18947	Aao18947 Human but
160	62	71.3	574	5	AAO18965	Aao18965 Human but
161	62	71.3	574	5	AAO18937	Aao18937 Human but
162	62	71.3	574	5	AAO18948	Aao18948 Human but
163	62	71.3	574	5	AAO18954	Aao18954 Human but
164	62	71.3	574	5	AAO18955	Aao18955 Human but
165	62	71.3	574	5	AAO18936	Aao18936 Human but
166	62	71.3	574	5	AAO18941	Aao18941 Human but
167	62	71.3	574	5	AAO18961	Aao18961 Human but
168	62	71.3	574	5	AAO18964	Aao18964 Human but
169	62	71.3	574	5	AAO18969	Aao18969 Human but
170	62	71.3	574	5	AAO18931	Aao18931 Human but
171	62	71.3	574	5	AAO18946	Aao18946 Human but
172	62	71.3	574	5	AAO18962	Aao18962 Human but
173	62	71.3	574	5	AAO18973	Aao18973 Human but
174	62	71.3	574	5	AAO18976	Aao18976 Human but
175	62	71.3	574	5	AAO18928	Aao18928 Human but
176	62	71.3	574	5	AAO18966	Aao18966 Human but
177	62	71.3	574	5	AAO18898	Aao18898 Human but
178	62	71.3	574	6	ABR62391	Abr62391 Human but
179	62	71.3	574	7	ABW00724	Abw00724 Human but
180	62	71.3	574	7	ABW00695	Abw00695 Human but
181	62	71.3	574	7	ABW00725	Abw00725 Human but
182	62	71.3	574	7	ABW00722	Abw00722 Human but
183	62	71.3	574	7	ABW00723	Abw00723 Human but
184	62	71.3	574	8	ADP44756	Adp44756 Human but
185	62	71.3	574	8	ADP44760	Adp44760 Human but
186	62	71.3	574	8	ADP44762	Adp44762 Human but
187	62	71.3	574	8	ADP44769	Adp44769 Human but
188	62	71.3	574	8	ADP44800	Adp44800 Human but
189	62	71.3	574	8	ADP44819	Adp44819 Human but
190	62	71.3	574	8	ADP44757	Adp44757 Human but
191	62	71.3	574	8	ADP44766	Adp44766 Human but
192	62	71.3	574	8	ADP44783	Adp44783 Human but
193	62	71.3	574	8	ADP44784	Adp44784 Human but
194	62	71.3	574	8	ADP44796	Adp44796 Human but
195	62	71.3	574	8	ADP44804	Adp44804 Human but
196	62	71.3	574	8	ADP44812	Adp44812 Human but
197	62	71.3	574	8	ADP44750	Adp44750 Human but
198	62	71.3	574	8	ADP44764	Adp44764 Human but
199	62	71.3	574	8	ADP44770	Adp44770 Human but
200	62	71.3	574	8	ADP44773	Adp44773 Human but
201	62	71.3	574	8	ADP44778	Adp44778 Human but
202	62	71.3	574	8	ADP44779	Adp44779 Human but
203	62	71.3	574	8	ADP44808	Adp44808 Human but
204	62	71.3	574	8	ADP44742	Adp44742 Human but
205	62	71.3	574	8	ADP44747	Adp44747 Human but
206	62	71.3	574	8	ADP44802	Adp44802 Human but
207	62	71.3	574	8	ADP44809	Adp44809 Human but
208	62	71.3	574	8	ADP44811	Adp44811 Human but
209	62	71.3	574	8	ADP44828	Adp44828 Human but
210	62	71.3	574	8	ADP44755	Adp44755 Human but
211	62	71.3	574	8	ADP44763	Adp44763 Human but
212	62	71.3	574	8	ADP44765	Adp44765 Human but
213	62	71.3	574	8	ADP44767	Adp44767 Human but
214	62	71.3	574	8	ADP44772	Adp44772 Human but
215	62	71.3	574	8	ADP44775	Adp44775 Human but
216	62	71.3	574	8	ADP44787	Adp44787 Human but
217	62	71.3	574	8	ADP44797	Adp44797 Human but
218	62	71.3	574	8	ADP44817	Adp44817 Human but
219	62	71.3	574	8	ADP44741	Adp44741 Human but
220	62	71.3	574	8	ADP44748	Adp44748 Human but
221	62	71.3	574	8	ADP44807	Adp44807 Human but
222	62	71.3	574	8	ADP44827	Adp44827 Human but
223	62	71.3	574	8	ADP44745	Adp44745 Human but
224	62	71.3	574	8	ADP44752	Adp44752 Human but
225	62	71.3	574	8	ADP44776	Adp44776 Human but
226	62	71.3	574	8	ADP44789	Adp44789 Human but
227	62	71.3	574	8	ADP44792	Adp44792 Human but
228	62	71.3	574	8	ADP44799	Adp44799 Human but
229	62	71.3	574	8	ADP44813	Adp44813 Human but
230	62	71.3	574	8	ADP44824	Adp44824 Human but
231	62	71.3	574	8	ADP44826	Adp44826 Human but
232	62	71.3	574	8	ADP44829	Adp44829 Human but
233	62	71.3	574	8	ADP44740	Adp44740 Human but
234	62	71.3	574	8	ADP44751	Adp44751 Human but
235	62	71.3	574	8	ADP44768	Adp44768 Human but
236	62	71.3	574	8	ADP44781	Adp44781 Human but
237	62	71.3	574	8	ADP44788	Adp44788 Human but
238	62	71.3	574	8	ADP44739	Adp44739 Human but
239	62	71.3	574	8	ADP44746	Adp44746 Human but
240	62	71.3	574	8	ADP44759	Adp44759 Human but
241	62	71.3	574	8	ADP44771	Adp44771 Human but
242	62	71.3	574	8	ADP44786	Adp44786 Human but
243	62	71.3	574	8	ADP44810	Adp44810 Human but
244	62	71.3	574	8	ADP44814	Adp44814 Human but

245	62	71.3	574	8	ADP44831	Adp44831 Human but	318	62	71.3	602	3	AAY49487	Aay49487 Human but
246	62	71.3	574	8	ADP44754	Adp44754 Human but	319	62	71.3	602	3	AAY49479	Aay49479 Human but
247	62	71.3	574	8	ADP44758	Adp44758 Human but	320	62	71.3	602	3	AAY49478	Aay49478 Human but
248	62	71.3	574	8	ADP44790	Adp44790 Human but	321	62	71.3	602	3	AAY49483	Aay49483 Human but
249	62	71.3	574	8	ADP44794	Adp44794 Human but	322	62	71.3	602	3	AAY49473	Aay49473 Human but
250	62	71.3	574	8	ADP44821	Adp44821 Human but	323	62	71.3	602	3	AAY49488	Aay49488 Human but
251	62	71.3	574	8	ADP44639	Adp44639 Human but	324	62	71.3	602	3	AAY49471	Aay49471 Human wil
252	62	71.3	574	8	ADP44743	Adp44743 Human but	325	62	71.3	602	3	AAY49475	Aay49475 Human but
253	62	71.3	574	8	ADP44749	Adp44749 Human but	326	62	71.3	602	3	AAY44573	Aay44573 Human wil
254	62	71.3	574	8	ADP44795	Adp44795 Human but	327	62	71.3	602	3	AAY44574	Aay44574 Human But
255	62	71.3	574	8	ADP44822	Adp44822 Human but	328	62	71.3	602	5	AAO18897	Aao18897 Human but
256	62	71.3	574	8	ADP44833	Adp44833 Human but	329	62	71.3	602	6	ABR62392	Abr62392 Human but
257	62	71.3	574	8	ADP44744	Adp44744 Human but	330	62	71.3	602	7	ADF90908	Adf90908 Human hep
258	62	71.3	574	8	ADP44774	Adp44774 Human but	331	62	71.3	635	1	AAP60097	Aap60097 Sequence
259	62	71.3	574	8	ADP44791	Adp44791 Human but	332	62	71.3	635	2	AAR41509	Aar41509 Full-leng
260	62	71.3	574	8	ADP44793	Adp44793 Human but	333	59	67.8	9	5	ABG66029	Abg66029 Human ace
261	62	71.3	574	8	ADP44816	Adp44816 Human but	334	59	67.8	10	5	ABG66038	Abg66038 Human ace
262	62	71.3	574	8	ADP44830	Adp44830 Human but	335	59	67.8	14	5	ABG65993	Abg65993 Human ace
263	62	71.3	574	8	ADP44761	Adp44761 Human but	336	59	67.8	40	4	AAG62386	Aag62386 Alternati
264	62	71.3	574	8	ADP44777	Adp44777 Human but	337	58	66.7	14	5	ABG66001	Abg66001 Human ace
265	62	71.3	574	8	ADP44782	Adp44782 Human but	338	58	66.7	42	4	AAU04300	Aau04300 Human but
266	62	71.3	574	8	ADP44823	Adp44823 Human but	339	58	66.7	42	4	AAG65954	Aag65954 Human but
267	62	71.3	574	8	ADP44738	Adp44738 Human but	340	57	65.5	43	4	AAU05014	Aau05014 Mouse but
268	62	71.3	574	8	ADP44801	Adp44801 Human but	341	57	65.5	43	4	AAG65956	Aag65956 Mouse but
269	62	71.3	574	8	ADP44820	Adp44820 Human but	342	57	65.5	47	4	AAU05013	Aau05013 Rabbit bu
270	62	71.3	574	8	ADP44785	Adp44785 Human but	343	57	65.5	47	4	AAG65955	Aag65955 Rabbit bu
271	62	71.3	574	8	ADP44798	Adp44798 Human but	344	56	64.4	574	5	AAO18904	Aao18904 Cat butyr
272	62	71.3	574	8	ADP44803	Adp44803 Human but	345	56	64.4	574	8	ADR01082	Adr01082 Cat butyr
273	62	71.3	574	8	ADP44815	Adp44815 Human but	346	55	63.2	14	5	ABG65994	Abg65994 Human ace
274	62	71.3	574	8	ADP44818	Adp44818 Human but	347	54	62.1	9	5	ABG66039	Abg66039 Human ace
275	62	71.3	574	8	ADP44825	Adp44825 Human but	348	48	55.2	8	5	ABG66030	Abg66030 Human ace
276	62	71.3	574	8	ADP44753	Adp44753 Human but	349	48	55.2	8	5	ABG66048	Abg66048 Human ace
277	62	71.3	574	8	ADP44780	Adp44780 Human but	350	48	55.2	14	5	ABG65995	Abg65995 Human ace
278	62	71.3	574	8	ADP44805	Adp44805 Human but	351	47	54.0	8	5	ABG66040	Abg66040 Human ace
279	62	71.3	574	8	ADP44806	Adp44806 Human but	352	47	54.0	100	2	AAY36833	Aay36833 Amino aci
280	62	71.3	574	8	ADR01039	Adr01039 Human but	353	47	54.0	583	8	ADJ93707	Adj93707 AChE1 pro
281	62	71.3	574	8	ADR01077	Adr01077 Human but	354	46	52.9	268	6	ABU12110	Abu12110 Human pro
282	62	71.3	574	8	ADR01051	Adr01051 Human but	355	45	51.7	440	6	ABO00551	Abo00551 Novel hum
283	62	71.3	574	8	ADR01059	Adr01059 Human but	356	45	51.7	824	3	AAB42174	Aab42174 Human ORF
284	62	71.3	574	8	ADR01055	Adr01055 Human but	357	44	50.6	7	5	ABG66031	Abg66031 Human ace
285	62	71.3	574	8	ADR01079	Adr01079 Human but	358	44	50.6	473	8	ADN20823	Adn20823 Bacterial
286	62	71.3	574	8	ADR01045	Adr01045 Butyrylch	359	43	49.4	7	5	ABG66041	Abg66041 Human ace
287	62	71.3	574	8	ADR01075	Adr01075 Human but	360	43	49.4	109	4	AAU60592	Aau60592 Propionib
288	62	71.3	574	8	ADR01053	Adr01053 Human but	361	43	49.4	109	6	ABM57111	Abm57111 Propionib
289	62	71.3	574	8	ADR01080	Adr01080 Human but	362	43	49.4	197	6	ABM69436	Abm69436 Photorhab
290	62	71.3	574	8	ADR01041	Adr01041 Human but	363	43	49.4	223	5	AAM49649	Aam49649 Human epi
291	62	71.3	574	8	ADR01047	Adr01047 Human but	364	43	49.4	496	4	ABG23733	Abg23733 Novel hum
292	62	71.3	574	8	ADR01057	Adr01057 Human but	365	43	49.4	585	5	ABB91077	Abb91077 Herbicida
293	62	71.3	574	8	ADR01063	Adr01063 Human but	366	43	49.4	593	4	ABB58290	Abb58290 Drosophil
294	62	71.3	574	8	ADR01067	Adr01067 Human but	367	42	48.3	67	4	AAU66113	Aau66113 Propionib
295	62	71.3	574	8	ADR01073	Adr01073 Human but	368	42	48.3	67	6	ABM62632	Abm62632 Propionib
296	62	71.3	574	8	ADR01061	Adr01061 Human but	369	42	48.3	119	6	ABO27172	Abo27172 Mouse ant
297	62	71.3	574	8	ADR01065	Adr01065 Human but	370	42	48.3	261	5	AAM49650	Aam49650 Canine ep
298	62	71.3	574	8	ADR01071	Adr01071 Human but	371	42	48.3	387	3	AAY99482	Aay99482 Jojoba ac
299	62	71.3	574	8	ADR01035	Adr01035 Human but	372	42	48.3	429	2	AAY60580	Aay60580 Human nor
300	62	71.3	574	8	ADR01043	Adr01043 Butyrylch	373	42	48.3	657	3	AAY52193	Aay52193 Beta gluc
301	62	71.3	574	8	ADR01081	Adr01081 Horse but	374	42	48.3	822	4	AAE01779	Aae01779 Human gen
302	62	71.3	574	8	ADR01037	Adr01037 Human but	375	42	48.3	822	4	AAE01851	Aae01851 Human gen
303	62	71.3	574	8	ADR01049	Adr01049 Human but	376	42	48.3	822	4	AAB47602	Aab47602 APC2. 1/2
304	62	71.3	574	8	ADR01069	Adr01069 Human but	377	42	48.3	822	5	ABG64185	Abg64185 Human alb
305	62	71.3	574	8	ADR01078	Adr01078 Human but	378	42	48.3	822	5	AAE24623	Aae24623 Human cul
306	62	71.3	602	2	AAR37442	Aar37442 Full-leng	379	42	48.3	822	6	ADA57244	Ada57244 Human sec
307	62	71.3	602	3	AAY49486	Aay49486 Human but	380	42	48.3	822	6	ADA41125	Ada41125 Human sec
308	62	71.3	602	3	AAY49481	Aay49481 Human but	381	42	48.3	822	7	ADC02487	Adc02487 Cullin AP
309	62	71.3	602	3	AAY59235	Aay59235 Human but	382	42	48.3	822	7	ADC74342	Adc74342 Human sec
310	62	71.3	602	3	AAY49472	Aay49472 Human but	383	42	48.3	822	7	ADF17872	Adf17872 Cullin AP
311	62	71.3	602	3	AAY49474	Aay49474 Human but	384	42	48.3	822	8	ADL77450	Adl77450 Albumin f
312	62	71.3	602	3	AAY49477	Aay49477 Human but	385	42	48.3	1578	7	ABM85515	Abm85515 Human pro
313	62	71.3	602	3	AAY49480	Aay49480 Human but	386	42	48.3	1784	8	ADF72342	Adf72342 Human sup
314	62	71.3	602	3	AAY49484	Aay49484 Human but	387	42	48.3	1788	2	AAY06077	Aay06077 Human act
315	62	71.3	602	3	AAY49485	Aay49485 Human but	388	42	48.3	1788	7	ADJ70459	Adj70459 Human hea
316	62	71.3	602	3	AAY49482	Aay49482 Human but	389	42	48.3	1789	7	ADE58829	Ade58829 Human Pro
317	62	71.3	602	3	AAY49476	Aay49476 Human but	390	42	48.3	1789	7	ADE58832	Ade58832 Human Pro

391	42	48.3	1792	2	AAY06078	Aay06078 Bovine ac
392	42	48.3	2152	7	ABM85514	Abm85514 Mouse pro
393	42	48.3	2213	2	AAY06079	Aay06079 Human act
394	41	47.1	73	4	AAM84033	Aam84033 Human imm
395	41	47.1	83	4	AAG76218	Aag76218 Human col
396	41	47.1	95	4	ABG03475	Abg03475 Novel hum
397	41	47.1	95	7	ADF60356	Adf60356 Human con
398	41	47.1	234	6	ABU24823	Abu24823 Protein e
399	41	47.1	327	4	AAB80415	Aab80415 Gene #1 a
400	41	47.1	349	4	AAB80414	Aab80414 Gene #1 a
401	41	47.1	358	6	ABM70568	Abm70568 Photorhab
402	41	47.1	414	4	AAB80371	Aab80371 Secreted
403	41	47.1	414	5	ABG65290	Abg65290 Human alb
404	41	47.1	414	6	ADA84087	Ada84087 Human HHL
405	41	47.1	414	8	ADL78557	Adl78557 Albumin f
406	41	47.1	414	8	ADQ80374	Adq80374 HERV-H LT
407	41	47.1	511	8	ADN10581	Adn10581 Nicotiana
408	41	47.1	511	8	ADN10583	Adn10583 Nicotiana
409	41	47.1	512	5	ABB91556	Abb91556 Herbicida
410	40.5	46.6	166	7	ADH86122	Adh86122 Enterococ
411	40.5	46.6	510	2	AAR41195	Aar41195 Yeast del
412	40.5	46.6	510	3	AAY70269	Aay70269 S. cerevi
413	40.5	46.6	510	8	ADS43511	Ads43511 Bacterial
414	40	46.0	6	5	ABG66032	Abg66032 Human ace
415	40	46.0	107	4	AAU52500	Aau52500 Propionib
416	40	46.0	107	6	ABM49019	Abm49019 Propionib
417	40	46.0	116	3	AAG24223	Aag24223 Arabidops
418	40	46.0	120	8	ADN48044	Adn48044 Thermococ
419	40	46.0	124	2	AAR15441	Aar15441 Heavy cha
420	40	46.0	124	2	AAR54244	Aar54244 Anti-HIV
421	40	46.0	124	2	AAR54245	Aar54245 Anti-HIV
422	40	46.0	124	2	AAR54246	Aar54246 Anti-HIV
423	40	46.0	124	2	AAR54335	Aar54335 Anti-HIV
424	40	46.0	124	2	AAR75568	Aar75568 VH Fab MT
425	40	46.0	124	2	AAW01246	Aaw01246 VH region
426	40	46.0	124	2	AAW01227	Aaw01227 VH region
427	40	46.0	124	2	AAW01309	Aaw01309 VH region
428	40	46.0	124	2	AAW01247	Aaw01247 VH region
429	40	46.0	124	3	AAY98207	Aay98207 Anti-gp12
430	40	46.0	124	3	AAY98206	Aay98206 Anti-gp12
431	40	46.0	124	3	AAY98208	Aay98208 Anti-gp12
432	40	46.0	124	3	AAY98270	Aay98270 Anti-gp12
433	40	46.0	124	3	AAY95097	Aay95097 Anti-gp12
434	40	46.0	124	3	AAY95098	Aay95098 Anti-gp12
435	40	46.0	124	3	AAY95161	Aay95161 Anti-gp12
436	40	46.0	124	3	AAY95099	Aay95099 Anti-gp12
437	40	46.0	124	6	AAE37618	Aae37618 Chimpanze
438	40	46.0	146	2	AAW01228	Aaw01228 VH region
439	40	46.0	146	3	AAY98285	Aay98285 Modified
440	40	46.0	146	3	AAY95176	Aay95176 Modified
441	40	46.0	146	7	ADE06734	Ade06734 Human IgG
442	40	46.0	186	8	ADK52392	Adk52392 Human ant
443	40	46.0	243	5	ABP45395	Abp45395 Human BLy
444	40	46.0	243	7	ADG96222	Adg96222 Single ch
445	40	46.0	247	5	ABP45373	Abp45373 Human BLy
446	40	46.0	247	7	ADG96200	Adg96200 Single ch
447	40	46.0	257	7	ADJ72368	Adj72368 Human ant
448	40	46.0	413	7	ADF05750	Adf05750 Bacterial
449	40	46.0	471	6	ABU19549	Abu19549 Protein e
450	40	46.0	476	7	ABR61564	Abr61564 Human MAb
451	40	46.0	549	4	ABB71550	Abb71550 Drosophil
452	40	46.0	587	8	ADH62812	Adh62812 Lactobaci
453	40	46.0	593	8	ADH62811	Adh62811 Lactobaci
454	40	46.0	735	7	ADM05741	Adm05741 Human pro
455	39.5	45.4	339	7	ADK19806	Adk19806 Human man
456	39.5	45.4	611	4	ABU52898	Abu52898 Human met
457	39.5	45.4	611	7	ADK19800	Adk19800 Human man
458	39.5	45.4	618	8	ADJ92351	Adj92351 Human N-l
459	39.5	45.4	6938	8	ADN96830	Adn96830 Bugula br
460	39	44.8	6	5	ABG66042	Abg66042 Human ace
461	39	44.8	68	4	AAM94177	Aam94177 Human rep
462	39	44.8	68	4	ABB95638	Abb95638 Human tes
463	39	44.8	96	4	AAM84483	Aam84483 Human imm
464	39	44.8	109	4	ABB11629	Abb11629 Human sec
465	39	44.8	112	4	ABG16780	Abg16780 Novel hum
466	39	44.8	116	7	ADB97826	Adb97826 HEV relat
467	39	44.8	121	7	ABG75311	Abg75311 Murine an
468	39	44.8	121	7	ABG75296	Abg75296 Murine mo
469	39	44.8	121	7	ABG75312	Abg75312 Murine an
470	39	44.8	121	7	ABG75315	Abg75315 Anti-CD22
471	39	44.8	121	7	ABG75313	Abg75313 Murine an
472	39	44.8	121	7	ABG75314	Abg75314 Murine an
473	39	44.8	121	8	ABM79524	Abm79524 Anti-CD22
474	39	44.8	121	8	ABM79525	Abm79525 Anti-CD22
475	39	44.8	121	8	ABM79526	Abm79526 Anti-CD22
476	39	44.8	121	8	ABM79527	Abm79527 Humanised
477	39	44.8	121	8	ABM79508	Abm79508 Murine an
478	39	44.8	121	8	ABM79523	Abm79523 Anti-CD22
479	39	44.8	124	2	AAR75612	Aar75612 VH Fab M5
480	39	44.8	124	2	AAR75572	Aar75572 VH Fab 3b
481	39	44.8	124	2	AAR75615	Aar75615 VH Fab M5
482	39	44.8	124	2	AAR75610	Aar75610 VH Fab M5
483	39	44.8	124	2	AAR75570	Aar75570 VH Fab 3b
484	39	44.8	124	2	AAR75611	Aar75611 VH Fab M5
485	39	44.8	124	2	AAR75617	Aar75617 VH Fab M5
486	39	44.8	124	2	AAR75613	Aar75613 VH Fab M5
487	39	44.8	124	2	AAR75616	Aar75616 VH Fab M5
488	39	44.8	124	2	AAR75614	Aar75614 VH Fab M5
489	39	44.8	137	2	AAR62445	Aar62445 81C6 heav
490	39	44.8	144	2	AAR08346	Aar08346 Heavy cha
491	39	44.8	151	4	AAG90539	Aag90539 C glutami
492	39	44.8	225	7	ABO84151	Abo84151 Pseudomon
493	39	44.8	231	6	ABU43347	Abu43347 Protein e
494	39	44.8	238	4	ABG24775	Abg24775 Novel hum
495	39	44.8	238	6	ABU30084	Abu30084 Protein e
496	39	44.8	238	7	ADC95792	Adc95792 E. faeciu
497	39	44.8	239	5	ABP39320	Abp39320 Staphyloc
498	39	44.8	250	3	AAY44346	Aay44346 3B3 antib
499	39	44.8	256	3	AAG09404	Aag09404 Arabidops
500	39	44.8	260	5	ABP45025	Abp45025 Human BLy

ALIGNMENTS

RESULT 1
AAW35340
ID AAW35340 standard; peptide; 14 AA.
XX
AC AAW35340;
XX
DT 17-APR-1998 (first entry)
XX
DE Human acetylcholinesterase 14-mer peptide.
XX
KW Acetylcholinesterase; AChE; neuronal degeneration; Parkinson's disease;
KW Alzheimer's disease; stroke; cancer; calcium channel modulator; antibody;
KW inhibitor.
XX
OS Homo sapiens.
XX
PN WO9735962-A1.
XX
PD 02-OCT-1997.
XX
PF 21-MAR-1997; 97WO-GB000796.
XX
PR 22-MAR-1996; 96GB-00006040.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Greenfield SA, Vaux DJ;
XX
DR WPI; 1997-489626/45.
XX
PT Peptide(s) from acetylcholine esterase which open calcium channels - used

PT for treating disorders of the central nervous system, cancer and stroke.
XX
PS Claim 1; Page 20; 27pp; English.
XX
CC This 14-mer peptide corresponds to residues 535-548 of the
CC Acetylcholinesterase mature protein. This peptide is known to act alone
CC or in synergism with a fragment of beta-amyloid to contribute to neuronal
CC degeneration. Compounds that inhibit the biological activity of the novel
CC peptides, and antibodies, can be used to control cytoplasmic calcium ion
CC currents in vivo, and are useful for treating disorders of the central
CC nervous system (e.g. Parkinson's and Alzheimer's diseases), stroke and
CC cancer
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 87; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
Db 1 AEFHRWSSYMVHWK 14

RESULT 2
AAU04701
ID AAU04701 standard; peptide; 14 AA.
XX
AC AAU04701;
XX
DT 26-SEP-2001 (first entry)
XX
DE Scrambled acetylcholinesterase (AChE) fragment.
XX
KW Acetylcholinesterase; AChE; neurodegenerative disease; brain;
KW neurological disorder; Alzheimer's disease; Parkinson's disease;
KW motor neuron disease; prion-related disease; NMDA; N-methyl-D-aspartate;
KW hippocampal dysfunction.
XX
OS Synthetic.
XX
PN WO200149107-A1.
XX
PD 12-JUL-2001.
XX
PF 22-DEC-2000; 2000WO-GB004991.
XX
PR 30-DEC-1999; 99GB-00030825.
XX
PA (SYNA-) SYNAPTICA LTD.
XX
PI Greenfield SA, Rawlins JNP, Deacon RMJ;
XX
DR WPI; 2001-441761/47.
XX
PT Providing animal model for Alzheimer's disease comprises introducing
PT peptide fragment from close to C-terminus of acetylcholine esterase which
PT causes cellular degeneration and impairment of testable brain function.
XX
PS Example 3; Page 25; 44pp; English.
XX
CC The sequence represents the amino acid sequence of a scrambled
CC acetylcholinesterase (AChE) fragment. The peptide is used in a method of
CC providing an animal model for a neurodegenerative disease. This involves
CC introducing the peptide fragment, from close to the C- terminus of AChE,
CC or an active variant of the peptide, into one or more sites in the brain
CC of a non-human animal, whereby the peptide causes cellular degeneration
CC and leads to impairment of testable brain function that is indicative of
CC a neurological disorder in a human. The animal model is useful for
CC testing an agent for biological activity in a neurodegenerative disorder
CC which involves administering the agent to a model for Alzheimer's disease
CC and determining whether the agent will inhibit, prevent or decrease
CC impairment of the testable brain function (cognitive function) and/or
CC cause improvement or deterioration of cellular damage in the brain. The
CC animal models are also useful as a model for Parkinson's disease, motor
CC neuron disease and prion-related diseases and thus for testing reagents
CC to asses their potential for treatment of Parkinson's disease. The AChE
CC peptide causes considerable nervous system damage, which is an order of
CC magnitude greater than that of the neurotoxin NMDA (N-methyl-D-
CC aspartate). The lesions produced can be identified using simple
CC behavioral tests known to be affected by hippocampal dysfunction
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 87; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
Db 1 AEFHRWSSYMVHWK 14

RESULT 3
ABG65979
ID ABG65979 standard; peptide; 14 AA.
XX
AC ABG65979;
XX
DT 28-AUG-2002 (first entry)
XX
DE Human acetylcholinesterase (AChE) Synaptica peptide.
XX
KW Human; acetylcholinesterase; Synaptica peptide; enzyme; AChE; amyloid;
KW acetylcholinesterase; fibril formation; surface tension; neuroprotective;
KW Alzheimer's disease; Parkinson's disease; motor neuron disease;
KW antiparkinsonian; nootropic.
XX
OS Homo sapiens.
XX
PN WO200242778-A2.
XX
PD 30-MAY-2002.
XX
PF 23-NOV-2001; 2001WO-GB005189.
XX
PR 23-NOV-2000; 2000GB-00028578.
XX
PA (SYNA-) SYNAPTICA LTD.
XX
PI Vaux DJT, Cottingham MG, Voskuil JLA;
XX
DR WPI; 2002-471743/50.
XX
PT Novel use of the 14 mer synaptica peptide, or its amyloidogenic variant
PT capable of fibril formation, in screening a compound for ability to
PT inhibit amyloid-type fibril formation by the peptide.
XX
PS Claim 1; Page 31; 41pp; English.
XX
CC The invention relates to use of the 14 mer Synaptica peptide (an active
CC fragment of acetylcholinesterase) or its amyloidogenic variant capable of
CC fibril formation, in screening a compound for ability to inhibit amyloid-
CC type fibril formation by the Synaptica peptide. The peptide is useful for
CC screening a compound for the ability to inhibit amyloid-type fibril
CC formation, for preparing a compound by identifying an inhibitor of fibril
CC formation and for determining whether a peptide or polypeptide or a
CC variant is an amyloidogenic analogue of the Synaptica peptide. The
CC peptide is also useful for determining whether variants will decrease
CC surface tension in aqueous solution. The compounds detected are used for
CC treating Alzheimer's disease, Parkinson's disease and motor neuron
CC disease. Sequences ABG65979-ABG66050 represent human Synaptica peptide
CC variants of the invention
XX
SQ Sequence 14 AA;

```
  Query Match             100.0%;  Score 87;  DB 5;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db          1 AEFHRWSSYMVHWK 14
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RESULT 4
AAR77010
ID   AAR77010 standard; protein; 39 AA.
XX
AC   AAR77010;
XX
DT   31-MAR-1996  (first entry)
XX
DE   Alternative human acetylcholinesterase (AChE) protein.
XX
KW   Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7; chromosome-7q22;
KW   acetylcholine-hydrolyzing enzyme.
XX
OS   Homo sapiens.
XX
PN   WO9523158-A1.
XX
PD   31-AUG-1995.
XX
PF   28-FEB-1995;   95WO-US002806.
XX
PR   28-FEB-1994;   94US-00202755.
PR   09-JAN-1995;   95US-00370156.
XX
PA   (YISS ) YISSUM RES & DEV CO.
PA   (KOHN/) KOHN K I.
XX
PI   Soreq H,  Zakut H,  Shani M;
XX
DR   WPI; 1995-311499/40.
XX
PT   Alternative forms of human acetyl cholinesterase (ChE) gene - expressed
PT   in transgenic animal assay system for evaluating anti-ChE activity of
PT   organo:phosphate(s), etc. or as model of ChE imbalance.
XX
PS   Disclosure; Fig 6; 55pp; English.
XX
CC   Human acetylcholinesterase (EC-3.1.1.7) is accumulated at neuromuscular
CC   junctions where it serves a vital function in modulating cholinergic
CC   neurotransmission. This alternatively spliced form of human AChE may be
CC   expressed in transgenic animals which are used in an assay system for
CC   determining the anti-ChE activity of organophosphates, carbamates, anti-
CC   ChE drugs, plant glycoalkaloids and snake venoms
XX
SQ   Sequence 39 AA;
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  Query Match             100.0%;  Score 87;  DB 2;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         11 AEFHRWSSYMVHWK 24
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RESULT 5
AAB48915
ID   AAB48915 standard; peptide; 40 AA.
XX
AC   AAB48915;
XX
DT   16-MAR-2001  (first entry)
XX
DE   Human acetylcholinesterase (AChE) C-terminal peptide, SEQ ID NO:2.
XX
KW   Acetylcholinesterase; AChE; splice variant; human; epitope;
KW   C-terminal peptide; antibody; central nervous system; CNS stress;
KW   psychological insult; physical insult; chemical insult;
KW   blood-brain barrier disruption; elevated glucocorticoid level;
KW   Alzheimer's disease; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO200073343-A2.
XX
PD   07-DEC-2000.
XX
PF   31-MAY-2000; 2000WO-IL000312.
XX
PR   31-MAY-1999;   99IL-00130225.
XX
PA   (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
PI   Soreq H,  Kaufer D,  Friedman A,  Seidman S;
XX
DR   WPI; 2001-061514/07.
XX
PT   Antibody specific to acetylcholinesterase or its C-terminal peptide
PT   derivative useful for diagnosing, ventral nervous system stress, elevated
PT   glucocorticoid level, disruption of blood-brain barrier and Alzheimer's
PT   disease.
XX
PS   Claim 4; Page 43; 44pp; English.
XX
CC   The invention relates to antibodies which recognise acetylcholinesterase
CC   (AChE) or a C-terminal peptide thereof (particularly AAB48914-B48916).
CC   The AChE splice variant, AChE-R, and AChE-R mRNA, have been found to be
CC   elevated in response to central nervous system (CNS) insults. The
CC   invention therefore also relates to a method for diagnosing CNS stress,
CC   and also elevated glucocorticoid levels, disruption of the blood-brain
CC   barrier or Alzheimer's disease using a sample (e.g., serum or
CC   cerebrospinal fluid) and an antibody of the invention. The CNS stress
CC   which may be diagnosed using the antibodies is preferably that caused by
CC   psychological insult, physical insult (head injury, head trauma, or
CC   exposure to irradiation) or chemical insult (exposure to insecticide or
CC   nerve gas). The present sequence represents a human AChE C-terminal
CC   peptide which is specifically claimed as an epitope which is recognised
CC   by an antibody of the invention
XX
SQ   Sequence 40 AA;
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```
  Query Match             100.0%;  Score 87;  DB 4;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         12 AEFHRWSSYMVHWK 25
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RESULT 6
AAB50033
ID   AAB50033 standard; peptide; 40 AA.
XX
AC   AAB50033;
XX
DT   14-MAR-2001  (first entry)
XX
DE   Acetylcholinesterase synaptic peptide ASP-1.
XX
KW   ASP-1; haemostatic; acetylcholinesterase; AChE; cell growth; human;
KW   cell differentiation; thrombocytopenia; post-irradiation condition;
KW   post-chemotherapy condition; blood loss; stress-induced male infertility.
XX
OS   Homo sapiens.
XX
PN   WO200073427-A2.
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XX
PD 07-DEC-2000.
XX
PF 31-MAY-2000; 2000WO-IL000311.
XX
PR 31-MAY-1999; 99IL-00130224.
PR 02-SEP-1999; 99IL-00131707.
XX
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
PI Soreq H, Eldor A, Deutch V, Grisaru D;
XX
DR WPI; 2001-061523/07.
XX
PT New regulatory peptides having cell growth and cell differentiation
PT activity derived from the C-terminal region of acetylcholinesterase
PT useful in promoting growth, survival and differentiation of stem cells.
XX
PS Claim 8; Page 50; 133pp; English.
XX
CC The present sequence is a C-terminal peptide of acetylcholinesterase
CC (AChE). This peptide is acetylcholinesterase "synaptic" peptide (ASP-1).
CC This peptide has a cell growth and/or cell differentiation activity. The
CC peptide may be used in ex vivo or in vivo expansion of haematopoietic
CC stem cells and neural progenitors, and in the promotion of megakaryocytic
CC differentiation of hematopoietic stem cells. In addition, the present
CC peptide may be used in for promoting expansion of committed neural
CC progenitors in a developing embryo, in cultured embryonic stem cells, and
CC embryoid bodies derived from them. The present peptide may further be
CC used in the treatment of thrombocytopenia, post-irradiation conditions,
CC post-chemotherapy conditions, and conditions following massive blood
CC loss, in inducing synthesis of AChE mRNA, and in promoting formation of
CC hematon bodies. Antibodies directed against the present peptide are
CC useful for diagnosing stress-induced male infertility
XX
SQ Sequence 40 AA;

Query Match 100.0%; Score 87; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 12 AEFHRWSSYMVHWK 25

RESULT 7
AAU98023
ID AAU98023 standard; peptide; 40 AA.
XX
AC AAU98023;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human synaptic acetylcholinesterase unique region.
XX
KW Human; acetylcholinesterase; single-chain variable fragment; synaptic;
KW scFv; AChE-S; heavy chain variable region; muscle re-innervation;
KW progressive neuromuscular disorder; muscle distortion; myasthenia gravis;
KW neuromuscular junction abnormality; Eaton-Lambert disease;
KW muscular dystrophy; amyotrophic lateral sclerosis; ALS;
KW post-traumatic stress disorder; PTSD; multiple sclerosis; Dystonia;
KW post-stroke sclerosis; post-injury muscle damage;
KW excessive re-innervation.
XX
OS Homo sapiens.
XX
PN WO200246422-A1.
XX
PD 13-JUN-2002.
XX
PF 22-MAY-2001; 2001WO-IL000464.
XX
PR 04-DEC-2000; 2000IL-00140071.
XX
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
PI Soreq H, Flores CF, Nissim A;
XX
DR WPI; 2002-463832/49.
XX
PT Nucleic acid sequence coding for a single-chain variable fragment (scFv)
PT antibody that has specific affinity for the synaptic variant of
PT acetylcholinesterase (AChE-S), useful for diagnosing a neuromuscular
PT disorder, e.g. Myasthenia gravis.
XX
PS Disclosure; Fig 1; 73pp; English.
XX
CC The invention relates to a nucleic acid sequence coding for a single-
CC chain variable fragment (scFv) antibody that has specific affinity for
CC the synaptic variant of acetylcholinesterase (AChE-S), where the scFv
CC antibody consists essentially of a polypeptide comprising the binding
CC portion of the heavy chain variable region of an antibody. Also included
CC are an expression vehicle comprising a nucleic acid sequence coding for a
CC scFv antibody that has specific affinity for the synaptic variant of AChE
CC -S, an scFv antibody specifically recognising and binding to the synaptic
CC variant of AChE-S and a method for the diagnosis of a progressive
CC neuromuscular disorder in a mammal, comprising obtaining a sample from
CC the mammal and detecting intensified expression of at least one of the
CC AChE variants in the sample. The single-chain Fv antibody is useful for
CC diagnosing a progressive neuromuscular disorder which involves any one of
CC muscle distortion, muscle re-innervation and neuromuscular junction (NMJ)
CC abnormalities. The disorder is Myasthenia gravis (preferred), Eaton-
CC Lambert disease, muscular dystrophy, amyotrophic lateral sclerosis (ALS),
CC post-traumatic stress disorder (PTSD), multiple sclerosis, Dystonia, post
CC -stroke sclerosis, post-injury muscle damage, excessive re-innervation,
CC or post-exposure to AChE inhibitors. The present sequence represents the
CC unique region of human acetylcholinesterase encoded by a synaptically
CC expressed splice variant
XX
SQ Sequence 40 AA;

Query Match 100.0%; Score 87; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 12 AEFHRWSSYMVHWK 25

RESULT 8
AAU04705
ID AAU04705 standard; peptide; 44 AA.
XX
AC AAU04705;
XX
DT 26-SEP-2001 (first entry)
XX
DE Rat acetylcholinesterase (AChE) fragment.
XX
KW Acetylcholinesterase; AChE; neurodegenerative disease; brain;
KW neurological disorder; Alzheimer's disease; Parkinson's disease;
KW motor neuron disease; prion-related disease; NMDA; N-methyl-D-aspartate;
KW hippocampal dysfunction; rat.
XX
OS Rattus sp.
XX
PN WO200149107-A1.
XX
PD 12-JUL-2001.
XX
PF 22-DEC-2000; 2000WO-GB004991.
XX
PR 30-DEC-1999; 99GB-00030825.
XX

```
PA   (SYNA-) SYNAPTICA LTD.
XX
PI   Greenfield SA,  Rawlins JNP,  Deacon RMJ;
XX
DR   WPI; 2001-441761/47.
XX
PT   Providing animal model for Alzheimer's disease comprises introducing
PT   peptide fragment from close to C-terminus of acetylcholine esterase which
PT   causes cellular degeneration and impairment of testable brain function.
XX
PS   Disclosure; Fig 1; 44pp; English.
XX
CC   The sequence represents the amino acid sequence of a biologically active
CC   fragment of rat acetylcholinesterase (AChE). The peptide is used in a
CC   method of providing an animal model for a neurodegenerative disease. This
CC   involves introducing the peptide fragment, from close to the C- terminus
CC   of AChE, or an active variant of the peptide, into one or more sites in
CC   the brain of a non-human animal, whereby the peptide causes cellular
CC   degeneration and leads to impairment of testable brain function that is
CC   indicative of a neurological disorder in a human. The animal model is
CC   useful for testing an agent for biological activity in a
CC   neurodegenerative disorder which involves administering the agent to a
CC   model for Alzheimer's disease and determining whether the agent will
CC   inhibit, prevent or decrease impairment of the testable brain function
CC   (cognitive function) and/or cause improvement or deterioration of
CC   cellular damage in the brain. The animal models are also useful as a
CC   model for Parkinson's disease, motor neuron disease and prion-related
CC   diseases and thus for testing reagents to asses their potential for
CC   treatment of Parkinson's disease. The AChE peptide causes considerable
CC   nervous system damage, which is an order of magnitude greater than that
CC   of the neurotoxin NMDA (N-methyl-D-aspartate). The lesions produced can
CC   be identified using simple behavioral tests known to be affected by
CC   hippocampal dysfunction
XX
SQ   Sequence 44 AA;

  Query Match             100.0%;  Score 87;  DB 4;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         16 AEFHRWSSYMVHWK 29


RESULT 9
AAU04704
ID   AAU04704 standard; peptide; 44 AA.
XX
AC   AAU04704;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Mouse acetylcholinesterase (AChE) fragment.
XX
KW   Acetylcholinesterase; AChE; neurodegenerative disease; brain;
KW   neurological disorder; Alzheimer's disease; Parkinson's disease;
KW   motor neuron disease; prion-related disease; NMDA; N-methyl-D-aspartate;
KW   hippocampal dysfunction; mouse.
XX
OS   Mus sp.
XX
PN   WO200149107-A1.
XX
PD   12-JUL-2001.
XX
PF   22-DEC-2000; 2000WO-GB004991.
XX
PR   30-DEC-1999;   99GB-00030825.
XX
PA   (SYNA-) SYNAPTICA LTD.
XX
PI   Greenfield SA,  Rawlins JNP,  Deacon RMJ;
XX
DR   WPI; 2001-441761/47.
XX
PT   Providing animal model for Alzheimer's disease comprises introducing
PT   peptide fragment from close to C-terminus of acetylcholine esterase which
PT   causes cellular degeneration and impairment of testable brain function.
XX
PS   Disclosure; Fig 1; 44pp; English.
XX
CC   The sequence represents the amino acid sequence of a biologically active
CC   fragment of mouse acetylcholinesterase (AChE). The peptide is used in a
CC   method of providing an animal model for a neurodegenerative disease. This
CC   involves introducing the peptide fragment, from close to the C- terminus
CC   of AChE, or an active variant of the peptide, into one or more sites in
CC   the brain of a non-human animal, whereby the peptide causes cellular
CC   degeneration and leads to impairment of testable brain function that is
CC   indicative of a neurological disorder in a human. The animal model is
CC   useful for testing an agent for biological activity in a
CC   neurodegenerative disorder which involves administering the agent to a
CC   model for Alzheimer's disease and determining whether the agent will
CC   inhibit, prevent or decrease impairment of the testable brain function
CC   (cognitive function) and/or cause improvement or deterioration of
CC   cellular damage in the brain. The animal models are also useful as a
CC   model for Parkinson's disease, motor neuron disease and prion-related
CC   diseases and thus for testing reagents to asses their potential for
CC   treatment of Parkinson's disease. The AChE peptide causes considerable
CC   nervous system damage, which is an order of magnitude greater than that
CC   of the neurotoxin NMDA (N-methyl-D-aspartate). The lesions produced can
CC   be identified using simple behavioral tests known to be affected by
CC   hippocampal dysfunction
XX
SQ   Sequence 44 AA;

  Query Match             100.0%;  Score 87;  DB 4;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         16 AEFHRWSSYMVHWK 29


RESULT 10
AAU04702
ID   AAU04702 standard; peptide; 44 AA.
XX
AC   AAU04702;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human acetylcholinesterase (AChE) fragment.
XX
KW   Acetylcholinesterase; AChE; neurodegenerative disease; brain;
KW   neurological disorder; Alzheimer's disease; Parkinson's disease;
KW   motor neuron disease; prion-related disease; NMDA; N-methyl-D-aspartate;
KW   hippocampal dysfunction; human.
XX
OS   Homo sapiens.
XX
PN   WO200149107-A1.
XX
PD   12-JUL-2001.
XX
PF   22-DEC-2000; 2000WO-GB004991.
XX
PR   30-DEC-1999;   99GB-00030825.
XX
PA   (SYNA-) SYNAPTICA LTD.
XX
PI   Greenfield SA,  Rawlins JNP,  Deacon RMJ;
XX
DR   WPI; 2001-441761/47.
XX
```

PT Providing animal model for Alzheimer's disease comprises introducing
PT peptide fragment from close to C-terminus of acetylcholine esterase which
PT causes cellular degeneration and impairment of testable brain function.
XX
PS Disclosure; Fig 1; 44pp; English.
XX
CC The sequence represents the amino acid sequence of a biologically active
CC fragment of human acetylcholinesterase (AChE). The peptide is used in a
CC method of providing an animal model for a neurodegenerative disease. This
CC involves introducing the peptide fragment, from close to the C- terminus
CC of AChE, or an active variant of the peptide, into one or more sites in
CC the brain of a non-human animal, whereby the peptide causes cellular
CC degeneration and leads to impairment of testable brain function that is
CC indicative of a neurological disorder in a human. The animal model is
CC useful for testing an agent for biological activity in a
CC neurodegenerative disorder which involves administering the agent to a
CC model for Alzheimer's disease and determining whether the agent will
CC inhibit, prevent or decrease impairment of the testable brain function
CC (cognitive function) and/or cause improvement or deterioration of
CC cellular damage in the brain. The animal models are also useful as a
CC model for Parkinson's disease, motor neuron disease and prion-related
CC diseases and thus for testing reagents to asses their potential for
CC treatment of Parkinson's disease. The AChE peptide causes considerable
CC nervous system damage, which is an order of magnitude greater than that
CC of the neurotoxin NMDA (N-methyl-D-aspartate). The lesions produced can
CC be identified using simple behavioral tests known to be affected by
CC hippocampal dysfunction
XX
SQ Sequence 44 AA;

Query Match 100.0%; Score 87; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 16 AEFHRWSSYMVHWK 29

RESULT 11
AAG65951
ID AAG65951 standard; protein; 44 AA.
XX
AC AAG65951;
XX
DT 11-FEB-2002 (first entry)
XX
DE Mouse acetylcholinesterase (AChE) partial sequence.
XX
KW Alpha 7 nicotinic receptor; acetylcholinesterase; AChE; synaptica;
KW antiparkinsonian; nootropic; neuroprotective; Alzheimer's disease;
KW Parkinson's disease; motor neuron disease.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 16. .29
FT /note= "synaptica peptide"
XX
PN WO200173446-A1.
XX
PD 04-OCT-2001.
XX
PF 29-MAR-2001; 2001WO-GB001401.
XX
PR 29-MAR-2000; 2000GB-00007630.
PR 15-DEC-2000; 2000GB-00030660.
XX
PA (SYNA-) SYNAPTICA LTD.
XX
PI Westwell M, Greenfield SA;
XX
DR WPI; 2001-639255/73.
XX
PT Use of alpha 7 nicotinic receptor or its functional analog to determine
PT if a compound is capable of acting as functional analog or antagonist of
PT acetylcholinesterase polypeptide for treating neurological disorders.
XX
PS Disclosure; Fig 1; 45pp; English.
XX
CC The invention relates to the use of an alpha 7 nicotinic receptor (I) or
CC its functional analog to determine whether a compound is capable of
CC acting as a functional analog or antagonist of an acetylcholinesterase
CC (AChE) polypeptide fragment (Synaptica peptide) on (I). If (I) is a
CC native alpha 7 nicotinic receptor in its normal membrane environment, it
CC is identified by means of inhibition by a blocker of (I). Methods for
CC identifying a functional analog or antagonist of the synaptica peptide
CC are also provided. The identified functional analog or antagonist is
CC useful for the preparation of a medicament for treatment of a
CC neurological disorder associated with non-enzymatic action of AChE, where
CC the neurological disorder is Alzheimer's disease, Parkinson's disease or
CC motor neuron disease. It is useful for inhibiting or preventing non-
CC enzymatic activity of the synaptica peptide in vivo. The present sequence
CC represents the partial sequence of mouse AChE polypeptide containing the
CC synaptica peptide fragment
XX
SQ Sequence 44 AA;

Query Match 100.0%; Score 87; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 9.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 16 AEFHRWSSYMVHWK 29

RESULT 12
AAG65949
ID AAG65949 standard; protein; 44 AA.
XX
AC AAG65949;
XX
DT 11-FEB-2002 (first entry)
XX
DE Human acetylcholinesterase (AChE) partial sequence.
XX
KW Alpha 7 nicotinic receptor; acetylcholinesterase; AChE; synaptica;
KW antiparkinsonian; nootropic; neuroprotective; Alzheimer's disease;
KW Parkinson's disease; motor neuron disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 16. .29
FT /note= "synaptica peptide"
XX
PN WO200173446-A1.
XX
PD 04-OCT-2001.
XX
PF 29-MAR-2001; 2001WO-GB001401.
XX
PR 29-MAR-2000; 2000GB-00007630.
PR 15-DEC-2000; 2000GB-00030660.
XX
PA (SYNA-) SYNAPTICA LTD.
XX
PI Westwell M, Greenfield SA;
XX
DR WPI; 2001-639255/73.
XX
PT Use of alpha 7 nicotinic receptor or its functional analog to determine
PT if a compound is capable of acting as functional analog or antagonist of
PT acetylcholinesterase polypeptide for treating neurological disorders.
XX

```
PS   Disclosure; Fig 1; 45pp; English.
XX
CC   The invention relates to the use of an alpha 7 nicotinic receptor (I) or
CC   its functional analog to determine whether a compound is capable of
CC   acting as a functional analog or antagonist of an acetylcholinesterase
CC   (AChE) polypeptide fragment (Synaptica peptide) on (I). If (I) is a
CC   native alpha 7 nicotinic receptor in its normal membrane environment, it
CC   is identified by means of inhibition by a blocker of (I). Methods for
CC   identifying a functional analog or antagonist of the synaptica peptide
CC   are also provided. The identified functional analog or antagonist is
CC   useful for the preparation of a medicament for treatment of a
CC   neurological disorder associated with non-enzymatic action of AChE, where
CC   the neurological disorder is Alzheimer's disease, Parkinson's disease or
CC   motor neuron disease. It is useful for inhibiting or preventing non-
CC   enzymatic activity of the synaptica peptide in vivo. The present sequence
CC   represents the partial sequence of human AChE polypeptide containing the
CC   synaptica peptide fragment
XX
SQ   Sequence 44 AA;

  Query Match             100.0%;  Score 87;  DB 4;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         16 AEFHRWSSYMVHWK 29


RESULT 13
AAG65952
ID   AAG65952 standard; protein; 44 AA.
XX
AC   AAG65952;
XX
DT   11-FEB-2002  (first entry)
XX
DE   Rat acetylcholinesterase (AChE) partial sequence.
XX
KW   Alpha 7 nicotinic receptor; acetylcholinesterase; AChE; synaptica;
KW   antiparkinsonian; nootropic; neuroprotective; Alzheimer's disease;
KW   Parkinson's disease; motor neuron disease.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         16. .29
FT                   /note= "synaptica peptide"
XX
PN   WO200173446-A1.
XX
PD   04-OCT-2001.
XX
PF   29-MAR-2001; 2001WO-GB001401.
XX
PR   29-MAR-2000; 2000GB-00007630.
PR   15-DEC-2000; 2000GB-00030660.
XX
PA   (SYNA-) SYNAPTICA LTD.
XX
PI   Westwell M,  Greenfield SA;
XX
DR   WPI; 2001-639255/73.
XX
PT   Use of alpha 7 nicotinic receptor or its functional analog to determine
PT   if a compound is capable of acting as functional analog or antagonist of
PT   acetylcholinesterase polypeptide for treating neurological disorders.
XX
PS   Disclosure; Fig 1; 45pp; English.
XX
CC   The invention relates to the use of an alpha 7 nicotinic receptor (I) or
CC   its functional analog to determine whether a compound is capable of
CC   acting as a functional analog or antagonist of an acetylcholinesterase
CC   (AChE) polypeptide fragment (Synaptica peptide) on (I). If (I) is a
CC   native alpha 7 nicotinic receptor in its normal membrane environment, it
CC   is identified by means of inhibition by a blocker of (I). Methods for
CC   identifying a functional analog or antagonist of the synaptica peptide
CC   are also provided. The identified functional analog or antagonist is
CC   useful for the preparation of a medicament for treatment of a
CC   neurological disorder associated with non-enzymatic action of AChE, where
CC   the neurological disorder is Alzheimer's disease, Parkinson's disease or
CC   motor neuron disease. It is useful for inhibiting or preventing non-
CC   enzymatic activity of the synaptica peptide in vivo. The present sequence
CC   represents the partial sequence of rat AChE polypeptide containing the
CC   synaptica peptide fragment
XX
SQ   Sequence 44 AA;

  Query Match             100.0%;  Score 87;  DB 4;  Length 44;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         16 AEFHRWSSYMVHWK 29


RESULT 14
AAW74586
ID   AAW74586 standard; protein; 45 AA.
XX
AC   AAW74586;
XX
DT   21-DEC-1998  (first entry)
XX
DE   Amino acid sequence of the human AChE variant 1.
XX
KW   Nuclease resistance; inhibition; human; acetyl-cholinesterase; AChE;
KW   central nervous system; CNS.
XX
OS   Homo sapiens.
XX
PN   WO9839486-A1.
XX
PD   11-SEP-1998.
XX
PF   06-MAR-1998;   98WO-US004503.
XX
PR   06-MAR-1997;   97US-0040203P.
XX
PA   (YISS ) YISSUM RES & DEV CO.
PA   (KOHN/) KOHN K I.
XX
PI   Soreq H,  Seidman S,  Shohami E;
XX
DR   WPI; 1998-506377/43.
XX
PT   Treatment of injury to central nervous system - by administration of
PT   inhibitor of acetyl-cholinesterase production.
XX
PS   Disclosure; Page 61; 88pp; English.
XX
CC   This is the amino acid sequence of a human acetyl-cholinesterase (AChE)
CC   variant used in the method of the invention, where inhibitors of AChE are
CC   used to treat injury to the central nervous system (CNS). The AChE
CC   inhibitor can also be used to facilitate transplantation of neuronal
CC   cells to the CNS of a patient. The inhibitor can also be used to improve
CC   hippocampal neuron survival following injury to the CNS. The CNS injuries
CC   that can be treated with the method include epilepsy, stroke,
CC   Huntington's disease, head injury, spinal injury, pain, Parkinson's
CC   disease, myelin deficiencies, neuromuscular disorders, neurological pain,
CC   amyotrophic lateral sclerosis, Alzheimer's disease, and affective
CC   disorders of the brain
XX
SQ   Sequence 45 AA;
```

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  Query Match             100.0%;  Score 87;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         17 AEFHRWSSYMVHWK 30
```

RESULT 15
AAW48800
ID AAW48800 standard; protein; 45 AA.
XX
AC AAW48800;
XX
DT 07-OCT-1998 (first entry)
XX
DE C-terminal fragment of human acetylcholine esterase variant E1-4,6.
XX
KW Human acetylcholine esterase-I4 readthrough splice variant; AChE-I4; CNS;
KW blood/brain barrier; BBB; I4 peptide; antibiotic; brain tumour; glioma;
KW chemotherapeutic drug; central nervous system.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Region   1. .5
FT   /note= "This region is encoded by the 3' end of AChE exon
FT   4"
FT Region   6. .45
FT   /note= "Residues encoded by AChE exon 6"
XX
PN WO9822132-A2.
XX
PD 28-MAY-1998.
XX
PF 20-NOV-1997; 97WO-US021696.
XX
PR 20-NOV-1996; 96US-0031194P.
PR 12-DEC-1996; 96US-0035266P.
PR 21-JUL-1997; 97US-0053200P.
XX
PA (YISS) YISSUM RES & DEV CO.
PA (KOHN/) KOHN K I.
XX
PI Soreq H, Friedman A, Seidman S, Kaufer D;
XX
DR WPI; 1998-312172/27.
XX
PT Increasing the permeability of the blood/brain barrier - using e.g.
PT adrenaline, atropine or acetylcholine esterase I4 splice variant peptide,
PT useful for imaging and/or treatment of central nervous system disorders.
XX
PS Disclosure; Fig 2; 71pp; English.
XX
CC The present sequence represents a C-terminal fragment of the human
CC acetylcholine esterase splice variant E1-4,6. The AChE E1-4,6 variant
CC comprises of residues encoded by exons 1-4 of AChE linked to residues
CC encoded by the alternatively spliced AChE exon 6. The invention claims
CC for the human acetylcholine esterase-I4 (AChE-I4) readthrough splice
CC variant (AAW48797). The invention provides a pharmaceutical composition,
CC for facilitating passage of compounds through the blood/brain barrier
CC (BBB), comprising of AChE-I4, I4 peptide (see AAW48797) or AChE-I4
CC analogues (such as the AChE E1-4,6 variant) together with a
CC pharmaceutically acceptable carrier. The pharmaceutical composition is
CC claimed to facilitate a reversible disruption of the BBB allowing
CC transport of compounds through the BBB. The compounds, e.g. imaging
CC agents, antibiotics or chemotherapeutic drugs, are claimed to be useful
CC for the diagnosis and treatment of diseases or disorders of the CNS such
CC as infections, neurochemical disorders, brain tumours, gliomas, etc
XX
SQ Sequence 45 AA;

```
  Query Match             100.0%;  Score 87;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         17 AEFHRWSSYMVHWK 30
```

RESULT 16
AAW68144
ID AAW68144 standard; protein; 45 AA.
XX
AC AAW68144;
XX
DT 05-OCT-1998 (first entry)
XX
DE Human AChE splice variant E1-4, 6.
XX
KW Nuclease resistant; acetylcholinesterase; human; myasthenia gravis; AChE;
KW Parkinson's disease; Alzheimer's disease; central nervous system;
KW neuromuscular junction; cholinergic signalling; brain.
XX
OS Homo sapiens.
XX
PN WO9826062-A2.
XX
PD 18-JUN-1998.
XX
PF 12-DEC-1997; 97WO-US023598.
XX
PR 12-DEC-1996; 96US-0035266P.
PR 13-FEB-1997; 97US-0037777P.
PR 02-MAY-1997; 97US-00850347.
PR 21-JUL-1997; 97US-0053334P.
XX
PA (YISS) YISSUM RES & DEV CO.
PA (KOHN/) KOHN K I.
XX
PI Soreq H, Seidman S, Eckstein F, Friedman A, Kaufer D;
XX
DR WPI; 1998-348522/30.
XX
PT Synthetic nuclease resistant antisense oligodeoxynucleotides - directed
PT against acetylcholinesterase, useful for treating Parkinson's and
PT Alzheimer's diseases and myasthenia gravis.
XX
PS Disclosure; Fig 12; 89pp; English.
XX
CC This represents the amino acid sequence of a human acetylcholinesterase
CC (AChE) splice variant. The invention provides sequences shown in AAV41278
CC to AAV41285 that represent synthetic nuclease resistant antisense
CC oligodeoxynucleotides which are capable of selectively modulating human
CC acetylcholinesterase (AChE) production. These oligonucleotides are
CC targeted to a splice junction in a splice variant of AChE mRNA and are
CC capable of selectively modulating human AChE production in the central
CC nervous system and neuromuscular junction. The invention also provides a
CC method for determining the efficacy of these human AChE specific
CC antisense oligonucleotides. These antisense oligonucleotides can be used
CC to restore balanced cholinergic signalling in the brain, particularly
CC related to learning and memory as well as stress disorders, Parkinson's
CC and Alzheimer's disease. They can also be used to reduce production and
CC therefore deposition of AChE in the neuromuscular junctions of patients
CC with e.g. myasthenia gravis. The oligonucleotides work effectively at low
CC doses while avoiding many of the side effects associated with Tacrine and
CC related cholinergic drugs for Alzheimer's disease and pyridostigmine and
CC related drugs for myasthenia gravis
XX
SQ Sequence 45 AA;

```
  Query Match             100.0%;  Score 87;  DB 2;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         17 AEFHRWSSYMVHWK 30


RESULT 17
AAU04299
ID   AAU04299 standard; peptide; 53 AA.
XX
AC   AAU04299;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Bovine acetylcholinesterase (AChE) fragment.
XX
KW   Acetylcholinesterase; AChE; neurodegenerative disease; brain;
KW   neurological disorder; Alzheimer's disease; Parkinson's disease;
KW   motor neuron disease; prion-related disease; NMDA; N-methyl-D-aspartate;
KW   hippocampal dysfunction; bovine.
XX
OS   Bos sp.
XX
PN   WO200149107-A1.
XX
PD   12-JUL-2001.
XX
PF   22-DEC-2000; 2000WO-GB004991.
XX
PR   30-DEC-1999;   99GB-00030825.
XX
PA   (SYNA-) SYNAPTICA LTD.
XX
PI   Greenfield SA,  Rawlins JNP,  Deacon RMJ;
XX
DR   WPI; 2001-441761/47.
XX
PT   Providing animal model for Alzheimer's disease comprises introducing
PT   peptide fragment from close to C-terminus of acetylcholine esterase which
PT   causes cellular degeneration and impairment of testable brain function.
XX
PS   Disclosure; Fig 1; 44pp; English.
XX
CC   The sequence represents the amino acid sequence of a biologically active
CC   fragment of bovine acetylcholinesterase (AChE). The peptide is used in a
CC   method of providing an animal model for a neurodegenerative disease. This
CC   involves introducing the peptide fragment, from close to the C-terminus
CC   of AChE, or an active variant of the peptide, into one or more sites in
CC   the brain of a non-human animal, whereby the peptide causes cellular
CC   degeneration and leads to impairment of testable brain function that is
CC   indicative of a neurological disorder in a human. The animal model is
CC   useful for testing an agent for biological activity in a
CC   neurodegenerative disorder which involves administering the agent to a
CC   model for Alzheimer's disease and determining whether the agent will
CC   inhibit, prevent or decrease impairment of the testable brain function
CC   (cognitive function) and/or cause improvement or deterioration of
CC   cellular damage in the brain. The animal models are also useful as a
CC   model for Parkinson's disease, motor neuron disease and prion-related
CC   diseases and thus for testing reagents to asses their potential for
CC   treatment of Parkinson's disease. The AChE peptide causes considerable
CC   nervous system damage, which is an order of magnitude greater than that
CC   of the neurotoxin NMDA (N-methyl-D-aspartate). The lesions produced can
CC   be identified using simple behavioral tests known to be affected by
CC   hippocampal dysfunction
XX
SQ   Sequence 53 AA;

  Query Match             100.0%;  Score 87;  DB 4;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         25 AEFHRWSSYMVHWK 38


RESULT 18
AAG65953
ID   AAG65953 standard; protein; 53 AA.
XX
AC   AAG65953;
XX
DT   11-FEB-2002  (first entry)
XX
DE   Bovine acetylcholinesterase (AChE) partial sequence.
XX
KW   Alpha 7 nicotinic receptor; acetylcholinesterase; AChE; synaptica;
KW   antiparkinsonian; nootropic; neuroprotective; Alzheimer's disease;
KW   Parkinson's disease; motor neuron disease.
XX
OS   Bos sp.
XX
FH   Key             Location/Qualifiers
FT   Peptide         25. .38
FT                   /note= "synaptica peptide"
XX
PN   WO200173446-A1.
XX
PD   04-OCT-2001.
XX
PF   29-MAR-2001; 2001WO-GB001401.
XX
PR   29-MAR-2000; 2000GB-00007630.
PR   15-DEC-2000; 2000GB-00030660.
XX
PA   (SYNA-) SYNAPTICA LTD.
XX
PI   Westwell M,  Greenfield SA;
XX
DR   WPI; 2001-639255/73.
XX
PT   Use of alpha 7 nicotinic receptor or its functional analog to determine
PT   if a compound is capable of acting as functional analog or antagonist of
PT   acetylcholinesterase polypeptide for treating neurological disorders.
XX
PS   Disclosure; Fig 1; 45pp; English.
XX
CC   The invention relates to the use of an alpha 7 nicotinic receptor (I) or
CC   its functional analog to determine whether a compound is capable of
CC   acting as a functional analog or antagonist of an acetylcholinesterase
CC   (AChE) polypeptide fragment (Synaptica peptide) on (I). If (I) is a
CC   native alpha 7 nicotinic receptor in its normal membrane environment, it
CC   is identified by means of inhibition by a blocker of (I). Methods for
CC   identifying a functional analog or antagonist of the synaptica peptide
CC   are also provided. The identified functional analog or antagonist is
CC   useful for the preparation of a medicament for treatment of a
CC   neurological disorder associated with non-enzymatic action of AChE, where
CC   the neurological disorder is Alzheimer's disease, Parkinson's disease or
CC   motor neuron disease. It is useful for inhibiting or preventing non-
CC   enzymatic activity of the synaptica peptide in vivo. The present sequence
CC   represents the partial sequence of bovine AChE polypeptide containing the
CC   synaptica peptide fragment
XX
SQ   Sequence 53 AA;

  Query Match             100.0%;  Score 87;  DB 4;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db         25 AEFHRWSSYMVHWK 38


RESULT 19
AAU04703
```

ID AAU04703 standard; peptide; 54 AA.
XX
AC AAU04703;
XX
DT 26-SEP-2001 (first entry)
XX
DE Rabbit acetylcholinesterase (AChE) fragment.
XX
KW Acetylcholinesterase; AChE; neurodegenerative disease; brain;
KW neurological disorder; Alzheimer's disease; Parkinson's disease;
KW motor neuron disease; prion-related disease; NMDA; N-methyl-D-aspartate;
KW hippocampal dysfunction; rabbit.
XX
OS Oryctolagus sp.
XX
PN WO200149107-A1.
XX
PD 12-JUL-2001.
XX
PF 22-DEC-2000; 2000WO-GB004991.
XX
PR 30-DEC-1999; 99GB-00030825.
XX
PA (SYNA-) SYNAPTICA LTD.
XX
PI Greenfield SA, Rawlins JNP, Deacon RMJ;
XX
DR WPI; 2001-441761/47.
XX
PT Providing animal model for Alzheimer's disease comprises introducing
PT peptide fragment from close to C-terminus of acetylcholine esterase which
PT causes cellular degeneration and impairment of testable brain function.
XX
PS Disclosure; Fig 1; 44pp; English.
XX
CC The sequence represents the amino acid sequence of a biologically active
CC fragment of rabbit acetylcholinesterase (AChE). The peptide is used in a
CC method of providing an animal model for a neurodegenerative disease. This
CC involves introducing the peptide fragment, from close to the C-terminus
CC of AChE, or an active variant of the peptide, into one or more sites in
CC the brain of a non-human animal, whereby the peptide causes cellular
CC degeneration and leads to impairment of testable brain function that is
CC indicative of a neurological disorder in a human. The animal model is
CC useful for testing an agent for biological activity in a
CC neurodegenerative disorder which involves administering the agent to a
CC model for Alzheimer's disease and determining whether the agent will
CC inhibit, prevent or decrease impairment of the testable brain function
CC (cognitive function) and/or cause improvement or deterioration of
CC cellular damage in the brain. The animal models are also useful as a
CC model for Parkinson's disease, motor neuron disease and prion-related
CC diseases and thus for testing reagents to asses their potential for
CC treatment of Parkinson's disease. The AChE peptide causes considerable
CC nervous system damage, which is an order of magnitude greater than that
CC of the neurotoxin NMDA (N-methyl-D-aspartate). The lesions produced can
CC be identified using simple behavioral tests known to be affected by
CC hippocampal dysfunction
XX
SQ Sequence 54 AA;

Query Match 100.0%; Score 87; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 26 AEFHRWSSYMVHWK 39

RESULT 20
AAG65950
ID AAG65950 standard; protein; 54 AA.
XX
AC AAG65950;
XX
DT 11-FEB-2002 (first entry)
XX
DE Rabbit acetylcholinesterase (AChE) partial sequence.
XX
KW Alpha 7 nicotinic receptor; acetylcholinesterase; AChE; synaptica;
KW antiparkinsonian; nootropic; neuroprotective; Alzheimer's disease;
KW Parkinson's disease; motor neuron disease.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT Peptide 26. .39
FT /note= "synaptica peptide"
XX
PN WO200173446-A1.
XX
PD 04-OCT-2001.
XX
PF 29-MAR-2001; 2001WO-GB001401.
XX
PR 29-MAR-2000; 2000GB-00007630.
PR 15-DEC-2000; 2000GB-00030660.
XX
PA (SYNA-) SYNAPTICA LTD.
XX
PI Westwell M, Greenfield SA;
XX
DR WPI; 2001-639255/73.
XX
PT Use of alpha 7 nicotinic receptor or its functional analog to determine
PT if a compound is capable of acting as functional analog or antagonist of
PT acetylcholinesterase polypeptide for treating neurological disorders.
XX
PS Disclosure; Fig 1; 45pp; English.
XX
CC The invention relates to the use of an alpha 7 nicotinic receptor (I) or
CC its functional analog to determine whether a compound is capable of
CC acting as a functional analog or antagonist of an acetylcholinesterase
CC (AChE) polypeptide fragment (Synaptica peptide) on (I). If (I) is a
CC native alpha 7 nicotinic receptor in its normal membrane environment, it
CC is identified by means of inhibition by a blocker of (I). Methods for
CC identifying a functional analog or antagonist of the synaptica peptide
CC are also provided. The identified functional analog or antagonist is
CC useful for the preparation of a medicament for treatment of a
CC neurological disorder associated with non-enzymatic action of AChE, where
CC the neurological disorder is Alzheimer's disease, Parkinson's disease or
CC motor neuron disease. It is useful for inhibiting or preventing non-
CC enzymatic activity of the synaptica peptide in vivo. The present sequence
CC represents the partial sequence of rabbit AChE polypeptide containing the
CC synaptica peptide fragment
XX
SQ Sequence 54 AA;

Query Match 100.0%; Score 87; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 26 AEFHRWSSYMVHWK 39

RESULT 21
AAB50037
ID AAB50037 standard; protein; 67 AA.
XX
AC AAB50037;
XX
DT 14-MAR-2001 (first entry)
XX
DE Acetylcholinesterase protein #2 used in a yeast two-hybrid system.
XX

KW ASP; haemostatic; acetylcholinesterase; AChE; cell growth; human;
KW cell differentiation; thrombocytopenia; post-irradiation condition;
KW post-chemotherapy condition; blood loss; stress-induced male infertility.
XX
OS Homo sapiens.
XX
PN WO200073427-A2.
XX
PD 07-DEC-2000.
XX
PF 31-MAY-2000; 2000WO-IL000311.
XX
PR 31-MAY-1999; 99IL-00130224.
PR 02-SEP-1999; 99IL-00131707.
XX
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
PI Soreq H, Eldor A, Deutch V, Grisaru D;
XX
DR WPI; 2001-061523/07.
XX
PT New regulatory peptides having cell growth and cell differentiation
PT activity derived from the C-terminal region of acetylcholinesterase
PT useful in promoting growth, survival and differentiation of stem cells.
XX
PS Claim 8; Page 87; 133pp; English.
XX
CC The present invention relates to C-terminal peptides of
CC acetylcholinesterase (AChE) (see AAB50032-B50034). The peptides of the
CC present invention have cell growth and/or cell differentiation activity.
CC The peptides may be used in ex vivo or in vivo expansion of
CC haematopoietic stem cells and neural progenitors, and in the promotion of
CC megakaryocytic differentiation of hematopoietic stem cells. In addition,
CC the peptides may be used in for promoting expansion of committed neural
CC progenitors in a developing embryo, in cultured embryonic stem cells, and
CC embryoid bodies derived from them. The peptides may further be used in
CC the treatment of thrombocytopenia, post-irradiation conditions, post-
CC chemotherapy conditions, and conditions following massive blood loss, in
CC inducing synthesis of AChE mRNA, and in promoting formation of hematon
CC bodies. Antibodies directed against the peptides are useful for
CC diagnosing stress-induced male infertility. The present sequence is a C-
CC terminal AChE "synaptic" protein (ASP), which was used in a yeast two-
CC hybrid system, to screen for ARP binding partners
XX
SQ Sequence 67 AA;

Query Match 100.0%; Score 87; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 39 AEFHRWSSYMVHWK 52

RESULT 22
ABG31332
ID ABG31332 standard; protein; 68 AA.
XX
AC ABG31332;
XX
DT 05-NOV-2002 (first entry)
XX
DE GFP-fused AChE variant expression construct, pGASP related protein.
XX
KW Nervous system; drug assay; acetylcholinesterase; AChE; brain;
KW isoform variance; AChE blocker; muscarinic receptor; M1; M2;
KW pyridostigmine; muscarinic receptor blocker; scopolamine;
KW M1 receptor blocker; pirenzepine; anxiety; post-traumatic stress;
KW Alzheimer's disease; muscle malfunctioning; neurodegenerative disorder;
KW xenobiotic damage; panic; neuromuscular disorder; Parkinson's disease;
KW Huntington's chorea; muscle fatigue; multiple chemical sensitivity;
KW autism; multiple sclerosis; Sjogren's disease; GFP; pGASP;
KW green fluorescent protein.
XX
OS Unidentified.
XX
PN WO200240994-A2.
XX
PD 23-MAY-2002.
XX
PF 14-NOV-2001; 2001WO-IL001051.
XX
PR 14-NOV-2000; 2000US-0247970P.
XX
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
PI Soreq H, Meshorer E, Sklan E, Shoham S;
XX
DR WPI; 2002-490152/52.
XX
PT Evaluating effect of drugs on nervous system by comparing effect of drug
PT on acetylcholinesterase, AChE activity in brain of test animal following
PT challenge by AChE blocker and comparing it with control group.
XX
PS Example; Page 52; 114pp; English.
XX
CC The present invention relates to a method and system for evaluating an
CC effect on the nervous system of a test drug. The method comprises
CC comparing the effect of the drug on acetylcholinesterase (AChE) catalytic
CC activity or isoform variance in a brain of a test animal following a
CC challenge by an AChE blocker or a blocker of AChE and muscarinic
CC receptors M1 and M2 (e.g. pyridostigmine) and comparing this effect with
CC that of a known agent, preferably a non-selective muscarinic receptor
CC blocker (e.g. scopolamine) or a specific M1 receptor blocker (e.g.
CC pirenzepine). The method is useful for evaluating an effect on the
CC nervous system of a test drug, including drugs for the treatment of
CC anxiety conditions, post-traumatic stress, Alzheimer's disease, muscle
CC malfunctioning, neurodegenerative disorders, damage resulting from
CC exposure to xenobiotics, panic, neuromuscular disorders, Parkinson's
CC disease, Huntington's chorea, muscle fatigue, multiple chemical
CC sensitivity, autism, multiple sclerosis and Sjogren's disease. The
CC present sequence represents a protein described in relation to green
CC fluorescent protein (GFP)-fused AChE variant expression construct pGASP
CC in the examples of the present invention
XX
SQ Sequence 68 AA;

Query Match 100.0%; Score 87; DB 5; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 40 AEFHRWSSYMVHWK 53

RESULT 23
ADL90218
ID ADL90218 standard; protein; 348 AA.
XX
AC ADL90218;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human enzyme, ENZM-28, SEQ ID 28.
XX
KW Cytostatic; Antiarteriosclerotic; Anticonvulsant; Nootropic;
KW Neuroprotective; Cerebroprotective; Anti-HIV; Antiallergic;
KW Antiinflammatory; Thyromimetic; Gene therapy; human; enzyme;
KW cell proliferative disorder; cancer; atherosclerosis;
KW neurological disorder; epilepsy; Huntington's disease; stroke;
KW immune disorder; inflammatory disorder; AIDS; allergies;
KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
KW ENZM-28.
XX

OS Homo sapiens.
XX
PN WO2004027022-A2.
XX
PD 01-APR-2004.
XX
PF 05-SEP-2003; 2003WO-US028177.
XX
PR 05-SEP-2002; 2002US-0408747P.
PR 28-OCT-2002; 2002US-0422062P.
PR 29-OCT-2002; 2002US-0422276P.
PR 13-DEC-2002; 2002US-0433328P.
PR 13-JAN-2003; 2003US-0439997P.
PR 15-JAN-2003; 2003US-0440850P.
PR 31-JAN-2003; 2003US-0444282P.
PR 04-FEB-2003; 2003US-0445371P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Sanjanwala MM, Lee S, Lee SY, Tran UK, Lu Y, Baughn MR;
PI Chawla NK, Lal PG, Ring HZ, Yang YG, Hafalia AJA, Yao MG;
PI Swarnakar A, Ison CH, Chang H, Ramkumar J, Khare R, Bhatia UG;
PI Burrill JD, Blake JJ, Ho A, Zheng W, Jiang X, Jackson AA;
PI Marquis JP, Jin P, Wilson AD, Favero KD, Wang JT, Becha SD;
PI Naidu S, Yue H, Griffin JA, Kable AE, Emerling BM, Lee EA, Tang YT;
PI Li JX, Forsythe IJ;
XX
DR WPI; 2004-295399/27.
DR N-PSDB; ADL90264.
XX
PT New human enzymes (ENZM), useful for diagnosing, treating and preventing
PT diseases or conditions associated with the aberrant ENZM expression e.g.
PT cancer, AIDS, epilepsy, or infections.
XX
PS Claim 1; SEQ ID NO 28; 344pp; English.
XX
CC The present invention relates to human enzymes (ENZM-1 - ENZM-46,
CC ADL90191-ADL90236) and their coding sequences (ADL90237-ADL90282). The
CC sequences are useful in diagnosing, treating and preventing diseases or
CC conditions associated with the decreased expression or overexpression of
CC the enzymes, such as cell proliferative (e.g. cancer, atherosclerosis),
CC neurological (e.g. epilepsy, Huntington's disease, stroke),
CC immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g.
CC Hypothyroidism, Cushing's syndrome) disorders, or infections.
XX
SQ Sequence 348 AA;

Query Match 100.0%; Score 87; DB 8; Length 348;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 320 AEFHRWSSYMVHWK 333

RESULT 24
ABM83175
ID ABM83175 standard; protein; 469 AA.
XX
AC ABM83175;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3424.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN41827.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 469 AA;

Query Match 100.0%; Score 87; DB 8; Length 469;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 441 AEFHRWSSYMVHWK 454

RESULT 25
AAR06990
ID AAR06990 standard; protein; 500 AA.
XX
AC AAR06990;
XX
DT 25-MAR-2003 (revised)
DT 16-JAN-1991 (first entry)
XX
DE Human foetal acetylcholinesterase (hAChE) primary transcript.
XX
KW Organophosphorous poisoning; OP; cancer; leukaemia; megakaryocytopoiesis;
KW ovarian cancer.
XX
OS Homo sapiens.
XX
PN EP388906-A.
XX

PD 26-SEP-1990.
XX
PF 20-MAR-1990; 90EP-00105274.
XX
PR 21-MAR-1989; 89IL-00089703.
XX
PA (YISS) YISSUM RES & DEV CO.
XX
PI Soreq H, Zakut H;
XX
DR WPI; 1990-291865/39.
DR N-PSDB; AAQ05999.
XX
PT Human acetyl:cholinesterase genetic molecules, peptide(s) - used for
PT organo-phosphorus poisoning, diagnosis or ovarian carcinoma(s) and haemo-
PT cytopoeitic, etc. disorders.
XX
PS Disclosure; Fig 1c; 47pp; English.
XX
CC Gene product is useful as an active pharmalogical component for the
CC prophylaxis and treatment of organophosphorous poisoning, and post-
CC surgical apnea due to succinylcholine administration. cDNA probe to the
CC sequence may be used in diagnosis of various leukaemias, abnormal
CC megakaryocytopoiesis and ovarian carcinomas. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 500 AA;

Query Match 100.0%; Score 87; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 472 AEFHRWSSYMVHWK 485

RESULT 26
ABR38991
ID ABR38991 standard; protein; 526 AA.
XX
AC ABR38991;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human acetylcholinesterase isomer protein #SEQ ID 2.
XX
KW Human; acetylcholinesterase; enzyme; AR-ACHE; cell withering.
XX
OS Homo sapiens.
XX
PN CN1376798-A.
XX
PD 30-OCT-2002.
XX
PF 23-MAR-2001; 2001CN-00105781.
XX
PR 23-MAR-2001; 2001CN-00105781.
XX
PA (SHAN-) SHANGHAI CELL BIOLOGY INST CHINESE ACAD.
XX
PI Zhang X, Yang L, He H;
XX
DR WPI; 2003-211570/21.
DR N-PSDB; ACC47509.
XX
PT Human acetylcholinesterase isomer protein (AR-ACHE) and its gene coding
PT sequence.
XX
PS Claim 3; Page 9 (disclosure); 19pp; Chinese.
XX
CC The invention relates to a novel human acetylcholinesterase isomer
CC protein (AR-ACHE) expressed when human tissue cells wither. Also
CC disclosed is the gene sequence encoding the protein. The cDNA is 1936 bp
CC in length and the protein is composed of 526 amino acid residues. The
CC process for preparing the protein and nucleic acid sequence, the process
CC for detecting the AR-ACHE nucleic acid sequence and polypeptide in a
CC sample, and the process for promoting or inhibiting cell withering are
CC also disclosed. The current sequence represents the human
CC acetylcholinesterase isomer protein amino acid sequence
XX
SQ Sequence 526 AA;

Query Match 100.0%; Score 87; DB 6; Length 526;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 498 AEFHRWSSYMVHWK 511

RESULT 27
ADR21588
ID ADR21588 standard; protein; 526 AA.
XX
AC ADR21588;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human enzyme ENZM-9 protein SEQ ID NO:9.
XX
KW human; enzyme; ENZM-9; immunosuppressive; antiinflammatory;
KW antimicrobial; neuroprotective; cardiovascular; ophthalmological;
KW gynaecological; cytostatic; gene therapy; immune deficiency;
KW autoimmune disorder; inflammatory disorder; infectious disorder;
KW neurological disorder; cardiovascular disorder; eye disorder;
KW metabolic disorder; reproductive disorder; cell proliferative disorder;
KW cancer.
XX
OS Homo sapiens.
XX
PN WO2004072267-A2.
XX
PD 26-AUG-2004.
XX
PF 12-FEB-2004; 2004WO-US004280.
XX
PR 12-FEB-2003; 2003US-0447246P.
PR 21-FEB-2003; 2003US-0449087P.
PR 26-FEB-2003; 2003US-0450622P.
PR 21-MAR-2003; 2003US-0456704P.
PR 15-APR-2003; 2003US-0463194P.
PR 09-MAY-2003; 2003US-0469358P.
PR 02-JUN-2003; 2003US-0475532P.
PR 04-JUN-2003; 2003US-0476278P.
PR 27-JUN-2003; 2003US-0483395P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Kable AE, Yue H, Baughn MR, Tribouley CM, Ring HZ, Tran UK;
PI Emerling BM, Ramkumar J, Hafalia AJA, Swarnakar A, Lee SY;
PI Chawla NK, Gietzen KJ, Marquis JP, Elliott VS, Becha SD, Favero KD;
PI Wang JT, Naidu S, Hawkins PR, Jin P, Chien D;
XX
DR WPI; 2004-625866/60.
DR N-PSDB; ADR21627.
XX
PT New enzymes, useful for diagnosing, treating, or preventing autoimmune,
PT inflammatory, infectious, neurological, cardiovascular, eye, metabolic,
PT reproductive, or cell proliferative disorders including cancer.
XX
PS Claim 1; SEQ ID NO 9; 305pp; English.
XX
CC The present sequence represents a human enzyme designated ENZM-9. Human
CC ENZM sequences have immunosuppressive, antiinflammatory, antimicrobial,

```
CC   neuroprotective, cardiovascular, ophthalmological, gynaecological and
CC   cytostatic activities, and can be used in gene therapy. The human ENZM
CC   polypeptides, polynucleotides, compositions, and methods of the present
CC   invention can be used for diagnosing, treating, or preventing immune
CC   deficiencies, or autoimmune, inflammatory, infectious, neurological,
CC   cardiovascular, eye, metabolic, reproductive, or cell proliferative
CC   disorders including cancer (e.g. breast, lung, colon, or ovarian cancer).
XX
SQ   Sequence 526 AA;

  Query Match             100.0%;  Score 87;  DB 8;  Length 526;
  Best Local Similarity   100.0%;  Pred. No. 0.00013;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        498 AEFHRWSSYMVHWK 511


RESULT 28
AAG80773
ID   AAG80773 standard; protein; 583 AA.
XX
AC   AAG80773;
XX
DT   19-APR-2002  (first entry)
XX
DE   AchE protein fragment #2.
XX
KW   AchE; acetylcholinesterase; ds.
XX
OS   Unidentified.
XX
PN   KR98077837-A.
XX
PD   16-NOV-1998.
XX
PF   23-APR-1997;   97KR-00015104.
XX
PR   23-APR-1997;   97KR-00015104.
XX
PA   (GLDS ) LG CHEM LTD.
XX
PI   Lee JH,  Kim CH,  Cho JM,  Yoon HS;
XX
DR   WPI; 2000-035682/03.
DR   N-PSDB; ABA97180.
XX
PT   Novel acetylcholinesterase gene and process for preparing
PT   acetylcholinesterase from E-coli using the same.
XX
PS   Disclosure; Page 17-19; 23pp; Korean.
XX
CC   This sequence represents the encoding nucleic fragment from
CC   acetylcholinesterase acid which is described in the disclosure of the
CC   invention
XX
SQ   Sequence 583 AA;

  Query Match             100.0%;  Score 87;  DB 3;  Length 583;
  Best Local Similarity   100.0%;  Pred. No. 0.00014;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        555 AEFHRWSSYMVHWK 568


RESULT 29
AAG80772
ID   AAG80772 standard; protein; 584 AA.
XX
AC   AAG80772;
XX
DT   19-APR-2002  (first entry)
XX
DE   AchE protein.
XX
KW   AchE; acetylcholinesterase.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 119
FT                   /note= "Encoded by TTC"
FT   Misc-difference 122
FT                   /note= "Encoded by GGT"
FT   Misc-difference 123
FT                   /note= "Encoded by GGC"
FT   Misc-difference 160
FT                   /note= "Encoded by CYG"
FT   Misc-difference 203
FT                   /note= "Encoded by GAG"
FT   Misc-difference 244
FT                   /note= "Encoded by GAG"
FT   Misc-difference 269
FT                   /note= "Encoded by GAG"
FT   Misc-difference 335
FT                   /note= "Encoded by GAF"
FT   Misc-difference 336
FT                   /note= "Encoded by FFC"
FT   Misc-difference 364
FT                   /note= "Encoded by GGT"
FT   Misc-difference 365
FT                   /note= "Encoded by GCG"
FT   Misc-difference 406
FT                   /note= "Encoded by CAA"
FT   Misc-difference 407
FT                   /note= "Encoded by CAT"
XX
PN   KR98077837-A.
XX
PD   16-NOV-1998.
XX
PF   23-APR-1997;   97KR-00015104.
XX
PR   23-APR-1997;   97KR-00015104.
XX
PA   (GLDS ) LG CHEM LTD.
XX
PI   Lee JH,  Kim CH,  Cho JM,  Yoon HS;
XX
DR   WPI; 2000-035682/03.
DR   N-PSDB; ABA97179.
XX
PT   Novel acetylcholinesterase gene and process for preparing
PT   acetylcholinesterase from E-coli using the same.
XX
PS   Disclosure; Page 13-15; 23pp; Korean.
XX
CC   This sequence represents a the acetylcholinesterase acid protein which is
CC   described in the disclosure of the invention
XX
SQ   Sequence 584 AA;

  Query Match             100.0%;  Score 87;  DB 3;  Length 584;
  Best Local Similarity   100.0%;  Pred. No. 0.00014;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        556 AEFHRWSSYMVHWK 569


RESULT 30
AAR06989
```

```
ID   AAR06989 standard; protein; 613 AA.
XX
AC   AAR06989;
XX
DT   25-MAR-2003  (revised)
DT   16-JAN-1991  (first entry)
XX
DE   Human acetylcholinesterase (hAChE) primary transcript.
XX
KW   Organophosphorous poisoning; OP; cancer; leukaemia; megakaryocytopoiesis;
KW   ovarian cancer.
XX
OS   Homo sapiens.
XX
PN   EP388906-A.
XX
PD   26-SEP-1990.
XX
PF   20-MAR-1990;   90EP-00105274.
XX
PR   21-MAR-1989;   89IL-00089703.
XX
PA   (YISS ) YISSUM RES & DEV CO.
XX
PI   Soreq H,  Zakut H;
XX
DR   WPI; 1990-291865/39.
DR   N-PSDB; AAQ05998.
XX
PT   Human acetyl:cholinesterase genetic molecules, peptide(s) - used for
PT   organo-phosphorus poisoning, diagnosis or ovarian carcinoma(s) and haemo-
PT   cytopoeitic, etc. disorders.
XX
PS   Claim 5; Page 25; 47pp; English.
XX
CC   Gene product is useful as an active pharmalogical component for the
CC   prophylaxis and treatment of organophosphorous poisoning, and post-
CC   surgical apnea due to succinylcholine administration. cDNA probe to the
CC   sequence may be used in diagnosis of various leukaemias, abnormal
CC   megakaryocytopoiesis and ovarian carcinomas. (Updated on 25-MAR-2003 to
CC   correct PA field.)
XX
SQ   Sequence 613 AA;

  Query Match             100.0%;  Score 87;  DB 2;  Length 613;
  Best Local Similarity   100.0%;  Pred. No. 0.00015;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        585 AEFHRWSSYMVHWK 598


RESULT 31
AAR80726
ID   AAR80726 standard; protein; 614 AA.
XX
AC   AAR80726;
XX
DT   31-MAR-1996  (first entry)
XX
DE   Human acetylcholinesterase (AChE) protein.
XX
KW   Acetylcholinesterase; acetyl cholinesterase; EC-3.1.1.7; chromosome-7q22;
KW   acetylcholine-hydrolyzing enzyme.
XX
OS   Homo sapiens.
XX
PN   WO9523158-A1.
XX
PD   31-AUG-1995.
XX
PF   28-FEB-1995;   95WO-US002806.
XX
PR   28-FEB-1994;   94US-00202755.
PR   09-JAN-1995;   95US-00370156.
XX
PA   (YISS ) YISSUM RES & DEV CO.
PA   (KOHN/) KOHN K I.
XX
PI   Soreq H,  Zakut H,  Shani M;
XX
DR   WPI; 1995-311499/40.
DR   N-PSDB; AAQ99002.
XX
PT   Alternative forms of human acetyl cholinesterase (ChE) gene - expressed
PT   in transgenic animal assay system for evaluating anti-ChE activity of
PT   organo:phosphate(s), etc. or as model of ChE imbalance.
XX
PS   Claim 3; Fig 1B; 55pp; English.
XX
CC   Human acetylcholinesterase (EC-3.1.1.7) is accumulated at neuromuscular
CC   junctions where it serves a vital function in modulating cholinergic
CC   neurotransmission. Alternatively spliced forms of human AChE may be
CC   expressed in transgenic animals which are used in an assay system for
CC   determining the anti-ChE activity of organophosphates, carbamates, anti-
CC   ChE drugs, plant glycoalkaloids and snake venoms
XX
SQ   Sequence 614 AA;

  Query Match             100.0%;  Score 87;  DB 2;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00015;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 32
AAY49490
ID   AAY49490 standard; protein; 614 AA.
XX
AC   AAY49490;
XX
DT   27-MAR-2000  (first entry)
XX
DE   Human acetylcholinesterase (AChE) mutant.
XX
KW   Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW   butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW   nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6001625-A.
XX
PD   14-DEC-1999.
XX
PF   19-MAY-1995;   95US-00446100.
XX
PR   19-MAY-1995;   95US-00446100.
XX
PA   (USSA ) US SEC OF ARMY.
XX
PI   Broomfield CA,  Lockridge O,  Millard CB;
XX
DR   WPI; 2000-096137/08.
XX
PT   Enhancing the organophosphate detoxifying capabilities of esterases for
PT   the treatment of organophosphate poisoning.
XX
PS   Disclosure; Col 13-14; 64pp; English.
XX
CC   The invention provides a method of enhancing organophosphate detoxifying
```

CC capabilities of esterases (either human acetylcholinesterases (AChE), human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that comprises substituting a histidine residue for 1 or more amino acid(s) within 6 Angstrom of an active site serine. The method may be used for enhancing organophosphate detoxifying capabilities of esterases (either human AChE, human BuChE and/or human CaE). The modified esterases may then be used to treat agricultural workers poisoned with organophosphates through contact with chemical such as sheep dips. They may also be used to treat military personnel contaminated by chemical weaponry such as nerve agents. Additionally, the esterases may also be used to decontaminate ground and buildings and equipment used to store, or contaminated by organophosphates. The method produces esterases with improved detoxification properties over naturally occurring organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also less likely to be inactivated by the OPAA
XX
SQ Sequence 614 AA;

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 586 AEFHRWSSYMVHWK 599

RESULT 33
AAY49489
ID AAY49489 standard; protein; 614 AA.
XX
AC AAY49489;
XX
DT 27-MAR-2000 (first entry)
XX
DE Human wild-type acetylcholinesterase (AChE).
XX
KW Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW nerve agent; organophosphorus acid anhydride; OPAA.
XX
OS Homo sapiens.
XX
PN US6001625-A.
XX
PD 14-DEC-1999.
XX
PF 19-MAY-1995; 95US-00446100.
XX
PR 19-MAY-1995; 95US-00446100.
XX
PA (USSA) US SEC OF ARMY.
XX
PI Broomfield CA, Lockridge O, Millard CB;
XX
DR WPI; 2000-096137/08.
XX
PT Enhancing the organophosphate detoxifying capabilities of esterases for
PT the treatment of organophosphate poisoning.
XX
PS Disclosure; Col 11-14; 64pp; English.
XX
CC The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE),
CC human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
CC comprises substituting a histidine residue for 1 or more amino acid(s)
CC within 6 Angstrom of an active site serine. The method may be used for
CC enhancing organophosphate detoxifying capabilities of esterases (either
CC human AChE, human BuChE and/or human CaE). The modified esterases may
CC then be used to treat agricultural workers poisoned with organophosphates
CC through contact with chemical such as sheep dips. They may also be used
CC to treat military personnel contaminated by chemical weaponry such as
CC nerve agents. Additionally, the esterases may also be used to
CC decontaminate ground and buildings and equipment used to store, or
CC contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA
XX
SQ Sequence 614 AA;

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 586 AEFHRWSSYMVHWK 599

RESULT 34
AAY49493
ID AAY49493 standard; protein; 614 AA.
XX
AC AAY49493;
XX
DT 27-MAR-2000 (first entry)
XX
DE Human acetylcholinesterase (AChE) mutant.
XX
KW Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6001625-A.
XX
PD 14-DEC-1999.
XX
PF 19-MAY-1995; 95US-00446100.
XX
PR 19-MAY-1995; 95US-00446100.
XX
PA (USSA) US SEC OF ARMY.
XX
PI Broomfield CA, Lockridge O, Millard CB;
XX
DR WPI; 2000-096137/08.
XX
PT Enhancing the organophosphate detoxifying capabilities of esterases for
PT the treatment of organophosphate poisoning.
XX
PS Disclosure; Col 15-16; 64pp; English.
XX
CC The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE),
CC human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
CC comprises substituting a histidine residue for 1 or more amino acid(s)
CC within 6 Angstrom of an active site serine. The method may be used for
CC enhancing organophosphate detoxifying capabilities of esterases (either
CC human AChE, human BuChE and/or human CaE). The modified esterases may
CC then be used to treat agricultural workers poisoned with organophosphates
CC through contact with chemical such as sheep dips. They may also be used
CC to treat military personnel contaminated by chemical weaponry such as
CC nerve agents. Additionally, the esterases may also be used to
CC decontaminate ground and buildings and equipment used to store, or
CC contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA
XX
SQ Sequence 614 AA;

Query Match 100.0%; Score 87; DB 3; Length 614;

```
  Best Local Similarity   100.0%;  Pred. No. 0.00015;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 35
AAY49492
ID   AAY49492 standard; protein; 614 AA.
XX
AC   AAY49492;
XX
DT   27-MAR-2000 . (first entry)
XX
DE   Human acetylcholinesterase (AChE) mutant.
XX
KW   Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW   butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW   nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6001625-A.
XX
PD   14-DEC-1999.
XX
PF   19-MAY-1995;   95US-00446100.
XX
PR   19-MAY-1995;   95US-00446100.
XX
PA   (USSA ) US SEC OF ARMY.
XX
PI   Broomfield CA,  Lockridge O,  Millard CB;
XX
DR   WPI; 2000-096137/08.
XX
PT   Enhancing the organophosphate detoxifying capabilities of esterases for
PT   the treatment of organophosphate poisoning.
XX
PS   Disclosure; Col 13-16; 64pp; English.
XX
CC   The invention provides a method of enhancing organophosphate detoxifying
CC   capabilities of esterases (either human acetylcholinesterases (AChE),
CC   human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
CC   comprises substituting a histidine residue for 1 or more amino acid(s)
CC   within 6 Angstrom of an active site serine. The method may be used for
CC   enhancing organophosphate detoxifying capabilities of esterases (either
CC   human AChE, human BuChE and/or human CaE). The modified esterases may
CC   then be used to treat agricultural workers poisoned with organophosphates
CC   through contact with chemical such as sheep dips. They may also be used
CC   to treat military personnel contaminated by chemical weaponry such as
CC   nerve agents. Additionally, the esterases may also be used to
CC   decontaminate ground and buildings and equipment used to store, or
CC   contaminated by organophosphates. The method produces esterases with
CC   improved detoxification properties over naturally occurring
CC   organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC   less likely to be inactivated by the OPAA
XX
SQ   Sequence 614 AA;

  Query Match             100.0%;  Score 87;  DB 3;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00015;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 36
```

```
AAY49491
ID   AAY49491 standard; protein; 614 AA.
XX
AC   AAY49491;
XX
DT   27-MAR-2000  (first entry)
XX
DE   Human acetylcholinesterase (AChE) mutant.
XX
KW   Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW   butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW   nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6001625-A.
XX
PD   14-DEC-1999.
XX
PF   19-MAY-1995;   95US-00446100.
XX
PR   19-MAY-1995;   95US-00446100.
XX
PA   (USSA ) US SEC OF ARMY.
XX
PI   Broomfield CA,  Lockridge O,  Millard CB;
XX
DR   WPI; 2000-096137/08.
XX
PT   Enhancing the organophosphate detoxifying capabilities of esterases for
PT   the treatment of organophosphate poisoning.
XX
PS   Disclosure; Col 13-14; 64pp; English.
XX
CC   The invention provides a method of enhancing organophosphate detoxifying
CC   capabilities of esterases (either human acetylcholinesterases (AChE),
CC   human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
CC   comprises substituting a histidine residue for 1 or more amino acid(s)
CC   within 6 Angstrom of an active site serine. The method may be used for
CC   enhancing organophosphate detoxifying capabilities of esterases (either
CC   human AChE, human BuChE and/or human CaE). The modified esterases may
CC   then be used to treat agricultural workers poisoned with organophosphates
CC   through contact with chemical such as sheep dips. They may also be used
CC   to treat military personnel contaminated by chemical weaponry such as
CC   nerve agents. Additionally, the esterases may also be used to
CC   decontaminate ground and buildings and equipment used to store, or
CC   contaminated by organophosphates. The method produces esterases with
CC   improved detoxification properties over naturally occurring
CC   organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC   less likely to be inactivated by the OPAA
XX
SQ   Sequence 614 AA;

  Query Match             100.0%;  Score 87;  DB 3;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00015;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 37
AAY49495
ID   AAY49495 standard; protein; 614 AA.
XX
AC   AAY49495;
XX
DT   27-MAR-2000  (first entry)
XX
DE   Human acetylcholinesterase (AChE) mutant.
XX
```

KW Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6001625-A.
XX
PD 14-DEC-1999.
XX
PF 19-MAY-1995; 95US-00446100.
XX
PR 19-MAY-1995; 95US-00446100.
XX
PA (USSA) US SEC OF ARMY.
XX
PI Broomfield CA, Lockridge O, Millard CB;
XX
DR WPI; 2000-096137/08.
XX
PT Enhancing the organophosphate detoxifying capabilities of esterases for
PT the treatment of organophosphate poisoning.
XX
PS Disclosure; Col 15-16; 64pp; English.
XX
CC The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE),
CC human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
CC comprises substituting a histidine residue for 1 or more amino acid(s)
CC within 6 Angstrom of an active site serine. The method may be used for
CC enhancing organophosphate detoxifying capabilities of esterases (either
CC human AChE, human BuChE and/or human CaE). The modified esterases may
CC then be used to treat agricultural workers poisoned with organophosphates
CC through contact with chemical such as sheep dips. They may also be used
CC to treat military personnel contaminated by chemical weaponry such as
CC nerve agents. Additionally, the esterases may also be used to
CC decontaminate ground and buildings and equipment used to store, or
CC contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA
XX
SQ Sequence 614 AA;

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 586 AEFHRWSSYMVHWK 599

RESULT 38
AAY49494
ID AAY49494 standard; protein; 614 AA.
XX
AC AAY49494;
XX
DT 27-MAR-2000 (first entry)
XX
DE Human acetylcholinesterase (AChE) mutant.
XX
KW Organophosphate; detoxification; esterase; acetylcholinesterase; AChE;
KW butrylcholinesterase; BuChE; carboxylesterase; CaE; sheep dip; human;
KW nerve agent; organophosphorus acid anhydride; OPAA; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6001625-A.
XX
PD 14-DEC-1999.
XX
PF 19-MAY-1995; 95US-00446100.
XX
PR 19-MAY-1995; 95US-00446100.
XX
PA (USSA) US SEC OF ARMY.
XX
PI Broomfield CA, Lockridge O, Millard CB;
XX
DR WPI; 2000-096137/08.
XX
PT Enhancing the organophosphate detoxifying capabilities of esterases for
PT the treatment of organophosphate poisoning.
XX
PS Disclosure; Col 15-16; 64pp; English.
XX
CC The invention provides a method of enhancing organophosphate detoxifying
CC capabilities of esterases (either human acetylcholinesterases (AChE),
CC human butrylcholinesterases (BuChE) and/or carboxylesterases (CaE)), that
CC comprises substituting a histidine residue for 1 or more amino acid(s)
CC within 6 Angstrom of an active site serine. The method may be used for
CC enhancing organophosphate detoxifying capabilities of esterases (either
CC human AChE, human BuChE and/or human CaE). The modified esterases may
CC then be used to treat agricultural workers poisoned with organophosphates
CC through contact with chemical such as sheep dips. They may also be used
CC to treat military personnel contaminated by chemical weaponry such as
CC nerve agents. Additionally, the esterases may also be used to
CC decontaminate ground and buildings and equipment used to store, or
CC contaminated by organophosphates. The method produces esterases with
CC improved detoxification properties over naturally occurring
CC organophosphorus acid anhydride (OPAA) hydrolyzing enzymes. They are also
CC less likely to be inactivated by the OPAA
XX
SQ Sequence 614 AA;

Query Match 100.0%; Score 87; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AEFHRWSSYMVHWK 14
||||||||||||||
Db 586 AEFHRWSSYMVHWK 599

RESULT 39
AAU11231
ID AAU11231 standard; protein; 614 AA.
XX
AC AAU11231;
XX
DT 26-FEB-2002 (first entry)
XX
DE Human acetylcholinesterase, ACHE.
XX
KW Human; ACHE; acetylcholinesterase; polymorphic variant; haplotyping;
KW genotyping; neurological disease; Parkinson's disease;
KW Alzheimer's disease; cancer; leukaemia; tumour; chromosome 7q22.
XX
OS Homo sapiens.
XX
PN WO200179219-A2.
XX
PD 25-OCT-2001.
XX
PF 11-APR-2001; 2001WO-US011853.
XX
PR 14-APR-2000; 2000US-0197173P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
PA (KAZE/) KAZEMI A.
XX
PI Bentivegna SC, Chew A, Choi JY, Koshy B;

```
XX
DR   WPI; 2002-055248/07.
DR   N-PSDB; AAS17492, AAS17493.
XX
PT   New polymorphic variants comprising acetylcholinesterase (ACHE) isogene,
PT   useful in expressing ACHE protein for use in screening for candidate
PT   drugs to treat diseases related to ACHE activity, e.g. neurological
PT   diseases or cancer.
XX
PS   Claim 29; Fig 2; 79pp; English.
XX
CC   The invention relates to a polynucleotide comprising a polymorphic
CC   variant of an acetylcholinesterase (ACHE) gene or fragment, protein or
CC   complement, the variant comprising an ACHE isogene defined by a haplotype
CC   selected from haplotypes 1-20 listed in the specification. Also included
CC   are methods for haplotyping and genotyping the ACHE gene of an
CC   individual, a method for predicting a haplotype pair for the ACHE gene of
CC   an individual, a method for identifying an association between a trait
CC   and at least one haplotype or haplotype pair of ACHE gene, recombinant
CC   nonhuman organisms transformed or transfected with the polynucleotide
CC   where the organism expresses ACHE protein encoded by the first nucleotide
CC   sequence or encoded by the polymorphic variant sequence, an isolated
CC   antibody specific for and immunoreactive with ACHE, a method of screening
CC   for drugs targeting the polypeptide contacting ACHE polymorphic variant
CC   with a candidate agent and assaying for binding activity, a computer
CC   system for storing and analysing polymorphism data for ACHE gene and a
CC   genome anthology for ACHE gene which comprises ACHE isogenes defined by
CC   haplotypes 1-20 given in the specification. The Polymorphisms are useful
CC   for studying the biological function of ACHE as well as in identifying
CC   drugs targeting this protein for the treatment of disorder related to its
CC   abnormal expression or function. The polymorphic variants may also be
CC   used in screening for compounds targeting ACHE to treat a specific
CC   condition or disease predicted to be associated with ACHE activity e.g.
CC   neurological diseases (e.g. Parkinson's disease and Alzheimer's disease),
CC   cancer, leukaemia, and tumours. The ACHE gene maps to human chromosome
CC   7q22. The present sequence is the ACHE protein
XX
SQ   Sequence 614 AA;

  Query Match             100.0%;  Score 87;  DB 5;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00015;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 40
AAU11232
ID   AAU11232 standard; protein; 614 AA.
XX
AC   AAU11232;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Human acetylcholinesterase, ACHE variant #1.
XX
KW   Human; ACHE; acetylcholinesterase; polymorphic variant; haplotyping;
KW   genotyping; neurological disease; Parkinson's disease;
KW   Alzheimer's disease; cancer; leukaemia; tumour; chromosome 7q22.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 34
FT                   /note= "Wild-type Arg substituted by Gln"
XX
PN   WO200179219-A2.
XX
PD   25-OCT-2001.
XX
PF   11-APR-2001; 2001WO-US011853.
XX
PR   14-APR-2000; 2000US-0197173P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
PA   (KAZE/) KAZEMI A.
XX
PI   Bentivegna SC,  Chew A,  Choi JY,  Koshy B;
XX
DR   WPI; 2002-055248/07.
XX
PT   New polymorphic variants comprising acetylcholinesterase (ACHE) isogene,
PT   useful in expressing ACHE protein for use in screening for candidate
PT   drugs to treat diseases related to ACHE activity, e.g. neurological
PT   diseases or cancer.
XX
PS   Claim 29; Page; 79pp; English.
XX
CC   The invention relates to a polynucleotide comprising a polymorphic
CC   variant of an acetylcholinesterase (ACHE) gene or fragment, protein or
CC   complement, the variant comprising an ACHE isogene defined by a haplotype
CC   selected from haplotypes 1-20 listed in the specification. Also included
CC   are methods for haplotyping and genotyping the ACHE gene of an
CC   individual, a method for predicting a haplotype pair for the ACHE gene of
CC   an individual, a method for identifying an association between a trait
CC   and at least one haplotype or haplotype pair of ACHE gene, recombinant
CC   nonhuman organisms transformed or transfected with the polynucleotide
CC   where the organism expresses ACHE protein encoded by the first nucleotide
CC   sequence or encoded by the polymorphic variant sequence, an isolated
CC   antibody specific for and immunoreactive with ACHE, a method of screening
CC   for drugs targeting the polypeptide contacting ACHE polymorphic variant
CC   with a candidate agent and assaying for binding activity, a computer
CC   system for storing and analysing polymorphism data for ACHE gene and a
CC   genome anthology for ACHE gene which comprises ACHE isogenes defined by
CC   haplotypes 1-20 given in the specification. The Polymorphisms are useful
CC   for studying the biological function of ACHE as well as in identifying
CC   drugs targeting this protein for the treatment of disorder related to its
CC   abnormal expression or function. The polymorphic variants may also be
CC   used in screening for compounds targeting ACHE to treat a specific
CC   condition or disease predicted to be associated with ACHE activity e.g.
CC   neurological diseases (e.g. Parkinson's disease and Alzheimer's disease),
CC   cancer, leukaemia, and tumours. The ACHE gene maps to human chromosome
CC   7q22. The present sequence is an ACHE protein polymorphic variant. Note:
CC   The present sequence is not shown in the specification but was created by
CC   the indexer from the ACHE sequence shown in figure 3 (AAU11231)
XX
SQ   Sequence 614 AA;

  Query Match             100.0%;  Score 87;  DB 5;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00015;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 41
AAU11234
ID   AAU11234 standard; protein; 614 AA.
XX
AC   AAU11234;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Human acetylcholinesterase, ACHE variant #3.
XX
KW   Human; ACHE; acetylcholinesterase; polymorphic variant; haplotyping;
KW   genotyping; neurological disease; Parkinson's disease;
KW   Alzheimer's disease; cancer; leukaemia; tumour; chromosome 7q22.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
```

```
FT   Misc-difference 353
FT                   /note= "Wild-type His substituted by Asn"
XX
PN   WO200179219-A2.
XX
PD   25-OCT-2001.
XX
PF   11-APR-2001; 2001WO-US011853.
XX
PR   14-APR-2000; 2000US-0197173P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
PA   (KAZE/) KAZEMI A.
XX
PI   Bentivegna SC,  Chew A,  Choi JY,  Koshy B;
XX
DR   WPI; 2002-055248/07.
XX
PT   New polymorphic variants comprising acetylcholinesterase (ACHE) isogene,
PT   useful in expressing ACHE protein for use in screening for candidate
PT   drugs to treat diseases related to ACHE activity, e.g. neurological
PT   diseases or cancer.
XX
PS   Claim 29; Page; 79pp; English.
XX
CC   The invention relates to a polynucleotide comprising a polymorphic
CC   variant of an acetylcholinesterase (ACHE) gene or fragment, protein or
CC   complement, the variant comprising an ACHE isogene defined by a haplotype
CC   selected from haplotypes 1-20 listed in the specification. Also included
CC   are methods for haplotyping and genotyping the ACHE gene of an
CC   individual, a method for predicting a haplotype pair for the ACHE gene of
CC   an individual, a method for identifying an association between a trait
CC   and at least one haplotype or haplotype pair of ACHE gene, recombinant
CC   nonhuman organisms transformed or transfected with the polynucleotide
CC   where the organism expresses ACHE protein encoded by the first nucleotide
CC   sequence or encoded by the polymorphic variant sequence, an isolated
CC   antibody specific for and immunoreactive with ACHE, a method of screening
CC   for drugs targeting the polypeptide contacting ACHE polymorphic variant
CC   with a candidate agent and assaying for binding activity, a computer
CC   system for storing and analysing polymorphism data for ACHE gene and a
CC   genome anthology for ACHE gene which comprises ACHE isogenes defined by
CC   haplotypes 1-20 given in the specification. The Polymorphisms are useful
CC   for studying the biological function of ACHE as well as in identifying
CC   drugs targeting this protein for the treatment of disorder related to its
CC   abnormal expression or function. The polymorphic variants may also be
CC   used in screening for compounds targeting ACHE to treat a specific
CC   condition or disease predicted to be associated with ACHE activity e.g.
CC   neurological diseases (e.g. Parkinson's disease and Alzheimer's disease),
CC   cancer, leukaemia, and tumours. The ACHE gene maps to human chromosome
CC   7q22. The present sequence is an ACHE protein polymorphic variant. Note:
CC   The present sequence is not shown in the specification but was created by
CC   the indexer from the ACHE sequence shown in figure 3 (AAU11231)
XX
SQ   Sequence 614 AA;

  Query Match             100.0%;  Score 87;  DB 5;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00015;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 42
AAU11233
ID   AAU11233 standard; protein; 614 AA.
XX
AC   AAU11233;
XX
DT   26-FEB-2002  (first entry)
XX
DE   Human acetylcholinesterase, ACHE variant #2.
XX
KW   Human; ACHE; acetylcholinesterase; polymorphic variant; haplotyping;
KW   genotyping; neurological disease; Parkinson's disease;
KW   Alzheimer's disease; cancer; leukaemia; tumour; chromosome 7q22.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 280
FT                   /note= "Wild-type Thr substituted by Ala"
XX
PN   WO200179219-A2.
XX
PD   25-OCT-2001.
XX
PF   11-APR-2001; 2001WO-US011853.
XX
PR   14-APR-2000; 2000US-0197173P.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
PA   (KAZE/) KAZEMI A.
XX
PI   Bentivegna SC,  Chew A,  Choi JY,  Koshy B;
XX
DR   WPI; 2002-055248/07.
XX
PT   New polymorphic variants comprising acetylcholinesterase (ACHE) isogene,
PT   useful in expressing ACHE protein for use in screening for candidate
PT   drugs to treat diseases related to ACHE activity, e.g. neurological
PT   diseases or cancer.
XX
PS   Claim 29; Page; 79pp; English.
XX
CC   The invention relates to a polynucleotide comprising a polymorphic
CC   variant of an acetylcholinesterase (ACHE) gene or fragment, protein or
CC   complement, the variant comprising an ACHE isogene defined by a haplotype
CC   selected from haplotypes 1-20 listed in the specification. Also included
CC   are methods for haplotyping and genotyping the ACHE gene of an
CC   individual, a method for predicting a haplotype pair for the ACHE gene of
CC   an individual, a method for identifying an association between a trait
CC   and at least one haplotype or haplotype pair of ACHE gene, recombinant
CC   nonhuman organisms transformed or transfected with the polynucleotide
CC   where the organism expresses ACHE protein encoded by the first nucleotide
CC   sequence or encoded by the polymorphic variant sequence, an isolated
CC   antibody specific for and immunoreactive with ACHE, a method of screening
CC   for drugs targeting the polypeptide contacting ACHE polymorphic variant
CC   with a candidate agent and assaying for binding activity, a computer
CC   system for storing and analysing polymorphism data for ACHE gene and a
CC   genome anthology for ACHE gene which comprises ACHE isogenes defined by
CC   haplotypes 1-20 given in the specification. The Polymorphisms are useful
CC   for studying the biological function of ACHE as well as in identifying
CC   drugs targeting this protein for the treatment of disorder related to its
CC   abnormal expression or function. The polymorphic variants may also be
CC   used in screening for compounds targeting ACHE to treat a specific
CC   condition or disease predicted to be associated with ACHE activity e.g.
CC   neurological diseases (e.g. Parkinson's disease and Alzheimer's disease),
CC   cancer, leukaemia, and tumours. The ACHE gene maps to human chromosome
CC   7q22. The present sequence is an ACHE protein polymorphic variant. Note:
CC   The present sequence is not shown in the specification but was created by
CC   the indexer from the ACHE sequence shown in figure 3 (AAU11231)
XX
SQ   Sequence 614 AA;

  Query Match             100.0%;  Score 87;  DB 5;  Length 614;
  Best Local Similarity   100.0%;  Pred. No. 0.00015;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 43
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```
ABP59222
ID   ABP59222 standard; protein; 614 AA.
XX
AC   ABP59222;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Human drug metabolising enzyme, DME-13, SEQ ID 13.
XX
KW   Human; drug metabolising enzyme; anti-HIV; antiallergic;
KW   antiinflammatory; antianaemic; thrombolytic; antilipaemic; antidiarrheic;
KW   antiarteriosclerotic; antiasthmatic; immunosuppressive; antithyroid;
KW   cytostatic; hepatotropic; virucide; dermatological; antidiabetic;
KW   nephrotropic; antigout; neuroprotective; thyromimetic; osteopathic;
KW   antiarthritic; antipsoriatic; uropathic; ophthalmological; antirheumatic;
KW   haemostatic; gene therapy; cell proliferative disorder; cancer;
KW   developmental disorder; endocrine disorder; eye disorder;
KW   metabolic disorder; gastrointestinal disorder; liver disorder;
KW   autoimmune disorder; inflammatory disorder; DME-13.
XX
OS   Homo sapiens.
XX
PN   WO2003004608-A2.
XX
PD   16-JAN-2003.
XX
PF   05-JUL-2002; 2002WO-US021105.
XX
PR   06-JUL-2001; 2001US-0303745P.
PR   13-JUL-2001; 2001US-0305402P.
PR   27-JUL-2001; 2001US-0308158P.
PR   14-SEP-2001; 2001US-0322127P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Griffin JA,  Ramkumar J,  Emerling BM,  Richardson TW,  Li JX;
PI   Warren BA,  Honchell CD,  Baughn MR,  Tang YT,  Lee EA,  Elliott VS;
PI   Yue H,  Lee S,  Swarnakar A,  Forsythe IJ,  Sanjanwala MM,  Yao MG;
PI   Zebarjadian Y,  Gorvad AE,  Becha SD,  Burford N;
XX
DR   WPI; 2003-221588/21.
DR   N-PSDB; ABZ81313.
XX
PT   New drug metabolizing enzymes (DME) useful for diagnosing, treating or
PT   preventing diseases or conditions associated with aberrant DME
PT   expression, e.g. cancer, AIDS, atherosclerosis, diabetes, glaucoma,
PT   hepatitis or osteoporosis.
XX
PS   Claim 1; Page 168-169; 181pp; English.
XX
CC   The present invention relates to novel human drug metabolising enzymes,
CC   DME-1 to DME-13 (ABP59210-ABP59222) and their coding sequences (ABZ81301-
CC   ABZ81313). The sequences are useful for diagnosing, treating or
CC   preventing disorders associated with aberrant expression of DME,
CC   particularly cell proliferative disorders (e.g. arteriosclerosis,
CC   atherosclerosis, cirrhosis, paroxysmal nocturnal haemoglobinuria,
CC   polycythaemia vera, psoriasis, primary thrombocytopenia or cancer),
CC   developmental disorders (e.g. renal tubular acidosis, anaemia or mental
CC   retardation), endocrine (e.g. osteoporosis, thrombosis, diabetes), eye
CC   disorders (e.g. glaucoma, keratitis), metabolic (e.g. hyperlipidaemia,
CC   cystic fibrosis), gastrointestinal disorders (e.g. gastroenteritis,
CC   diarrhoea), liver disorders (e.g. hepatitis, Reye's syndrome), or
CC   autoimmune/inflammatory disorders (e.g. AIDS, allergies, asthma,
CC   autoimmune thyroiditis, contact dermatitis, Crohn's disease,
CC   glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease,
CC   Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis,
CC   osteoarthritis, pancreatitis, Reiter's syndrome, rheumatoid arthritis,
CC   Sjogren's syndrome, uveitis). They are also useful in the assessing the
CC   effects of exogenous compounds on the expression of nucleic acid and
CC   amino acid sequences of DME. The polynucleotides encoding DME are useful
CC   for creating transgenic animals to model human disease
XX
SQ   Sequence 614 AA;

  Query Match           100.0%;  Score 87;  DB 6;  Length 614;
  Best Local Similarity  100.0%;  Pred. No. 0.00015;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


RESULT 44
ABB99726
ID   ABB99726 standard; protein; 614 AA.
XX
AC   ABB99726;
XX
DT   24-MAR-2003  (first entry)
XX
DE   Amino acid sequence of human acetylcholinesterase (YT blood group).
XX
KW   G protein-coupled receptor; GPCR; single cell biosensor; arrestin;
KW   GPCR ligand; muscarinic receptor; acetylcholinesterase; YT blood group.
XX
OS   Homo sapiens.
XX
PN   WO200299381-A2.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-2002; 2002WO-US017606.
XX
PR   05-JUN-2001; 2001US-0295945P.
PR   04-JUN-2002; 2002US-00161916.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Barak LS,  Shetzline MA,  Oakley RH,  Caron MG;
XX
DR   WPI; 2003-140644/13.
DR   N-PSDB; ABZ23128.
XX
PT   Novel single cell biosensor, useful for detecting G protein-coupled
PT   receptor ligand in a sample, comprises cell overexpressing arrestin and G
PT   protein-coupled receptor.
XX
PS   Disclosure; Fig 3E; 103pp; English.
XX
CC   The present sequence represents human acetylcholinesterase (YT blood
CC   group). Single cell biosensors of the invention which overexpress the
CC   muscarinic receptor are used to detect acetylcholinesterase inhibition.
CC   The muscarinic receptor is a G protein-coupled receptor (GPCR) that
CC   translocates arrestins. The specification describes a single cell
CC   biosensor comprising a cell which overexpresses arrestin and at least one
CC   GPCR, where the GPCR, the arrestin or the cell is detectably labeled for
CC   monitoring internalisation of the GPCR. The biosensor detects various
CC   bioreactive ligand species in the sample, as opposed to other antibody-
CC   based methods, such as radioimmunoassay, which detects only the ligand
CC   species with the reactive epitope. The biosensor is useful for detecting
CC   a GPCR ligand in a test sample, for monitoring a GPCR ligand in a mammal,
CC   for detecting a compound which modulates a GPCR ligand in a test sample,
CC   for continuous screening of GPCR ligands in a test sample, and for
CC   detecting a compound that modulates GPCR internalisation in a test
CC   sample. It is useful for altering GPCR internalisation. It is also useful
CC   for detecting an inhibitor of acetylcholinesterase in a test sample
XX
SQ   Sequence 614 AA;

  Query Match           100.0%;  Score 87;  DB 6;  Length 614;
  Best Local Similarity  100.0%;  Pred. No. 0.00015;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
```

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Db        586 AEFHRWSSYMVHWK 599

RESULT 45
ADE61695
ID   ADE61695 standard; protein; 614 AA.
XX
AC   ADE61695;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Rat Protein AAB24586, SEQ ID NO 7617.
XX
KW   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW   chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS   Rattus norvegicus.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; AAB24586.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a rat protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 614 AA;

  Query Match            100.0%;  Score 87;  DB 7;  Length 614;
  Best Local Similarity  100.0%;  Pred. No. 0.00015;
    Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AEFHRWSSYMVHWK 14
              ||||||||||||||
Db        586 AEFHRWSSYMVHWK 599


Search completed: October 12, 2005, 10:22:58
Job time : 175 secs
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